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GenCore version 5.1.6
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Copyright (c) 1993 - 2003 Compugen Ltd.	OM nucleic - nucleic search, using sw model	Run on: November 25, 2003, 22:28:25; Search time 5208.63 Seconds (without alignments) 16556.656 Million cell updates/sec	Title: US-09-852-209A-2 Perfect score: 2108 Sequence: 1 ccccgccgtgagtgagtctctncttttttgaaaataattaa 2108	Scoring table: IDENTITY NUC Gapext 1.0	Searched: 2888711 seqs, 20454813386 residues	Total number of hits satisfying chosen parameters: 5777422	Minimum DB seq length: 0 Maximum DB seq length: 2000000000	Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries	:* ''' ''' ''' ''' ''' ''' '''		200
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total ecora direction.

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ALIGNMENTS

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. 4	derived growth	ı				ordata; Craniat	imates; Catarrh		K., Karlsson, I	m, M., Bostrom, F	H., Alitalo, K
ç	AF244613 Homo sapiens platelet-derived growth factor C mRNA, complete cds.	AF244813 AF244813.1 GI:8886883		Homo sapiens (human)	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.	1 (bases 1 to 2152)	Li, X., Ponten, A., Aase, K., Karlsson, L., Abramsson, A., Uutela, M.,	rom, G., Hellstro	ltz,C., Heldin,C
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RESULT 1 AF244813	DEFINITION	ACCESSION VERSION	KEYWORDS	SOURCE	ORGANISM			REFERENCE	AUTHORS		

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                          541 GAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAAT 600
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NIVMPQFTEAVSPSVLPPSALPLDILMNAITAFSTLEDLIRYLEPERWQLDLEDLYRP
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VKRCGGNCACCLHACNECQCVPSKVTXKYHEVLQLRPKTGVRGLHKSLTDVALEHHEB
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factor receptor alpha (PDGRA1pha)"
factor receptor alpha (PDGFVDEF growth factor
family; contains N-terminal CUB domain and the C-terminal
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                                                                                                         [Dases 1 to 2152]
Briksson, U., Aase, K., Li, X. and Ponten, A.
Direct Submission
Submitted (14-MAR-2000) Ludwig Institute for Cancer Research, Nobels vag 3 P.O. Box 240, Stockholm S-171 77, Sweden
Location/Qualifiers
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PDGF-C is a new protease-activated ligand for the PDGF
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/product="platelet-derived growth factor C"
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                                        Nat. Cell Biol. 2 (5), 302-309 (2000)
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/db_xref="taxon:9606"
/tissue_type="lung"
/dev_stage="fetal"
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BASE COUNT 849 a 522 c 605 g 848 t 1 others	Query Match 93.9%; Score 1979.4; DB 6; Length 2825; Best Local Similarity 97.7%; Pred. No. 0; Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5;	Fr4 Fr4	28 62	122	Qy 182 TIBITACIGITCIACIAALGGAAGIATICACAGCCCAAGGITICCICATACITATCCAA 241 Dh 40.4 TIBITATACAAGAAGAAGAACATATCCTCATACATACTTATCCAA 463	242 GAAATACGGTCTTGGTATGGAGATTAGTAGAGGAGTAGAGGAAAATGTATGGATACAACTTA 464 GAAATACGGTCTTGGTATGGAGTAGAGAGAGAAAATGTATGGATACAACTTA	302 CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTTTTG 504 CGTTTGATGAAGATTTGGGCTTTGAAGACCCAGAAGATGACATATGCAAGTTTTG 504 CGTTTGATGAAGATTTGGGCTTTGAAGACCCAGAAGATGAAGATTTTG	362 TAGAAGTTGAGGAACCCAGGGAACTATATTAGGGCGCTGGTGGGTACTGGTACTGGTACTGGTACTGGTAACTATAATAGGCCCTGGTGGTACTACTACTACTACTACTACTACTACTACTACTACTACT	422 TACCAGGAAAAGAGTTTCTAAAGGAATCAAATTAGGATAAGATTTGTATCTGATGAAT 644 TACCAGGAAAAAGAATTAGAAATTAGAATTAGATTAGTATCTGATGAAT	482 ATTICCITCIBACCAGGGTTCACATCACATACAACATGCAATTGCACAATTCACAGGGTTCACAGGGTTCACAACAATTGCAAATTCACAGGTTCACAGGGTTCACAAAAAAAA	542 AAGCTGTGAGTCCTTCAGTGCTACCCCTTTCACCTTTGCCACTGGACCTGCTTAATAATG [662 AGTTGGACTTAGAAGATCTATAGGCCAACTTGGACCAAGGCGTTTGTTT	Qy 722 TIGGAAGAAATCCAGAGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 781	182	Oy 842 TITICIGACCAGGITGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTCTCC 901	902 ACATICCAATGAATGAATGATGCCCAAGGAAGTTACTAAAAAATACCAGGAGGCCC	Db 1124 ACATTGCAATGTGTGTGTGTGTCCCAAAGCAAAGTACAAATCCAAGAGGTCC 1183 Ov 962 TTCAGTGTGAATGAAGTGTGTGTCAAGCAAAGCAAAATACCAAGAGGTCC 1031	
	acaggaaaaaactg acaggaaaaaactg	1442 TGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGTCCTCGTGCTCGGGCCT 1501	1502 AAAATGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTGACATATGTAAAACC 1561 	1562 agaacattctatgtactacaacctggtttttaaaaggaactatgttgctatgaattaa 1621 	1622 ACTIGIGICRIGCIGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAATTTCTGCC 1681 	1682 atttagaagaagaactacattcatggtttggaagagataacctgaaaagaagaggg 1741 	1742 CCTTAICTTCACTTTAICGATAAGTCAGTTTATTIGTTICATIGTGTACATTTTTATATT 1801 	1802 CTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACC 1861 	1862 AAAGGTATTTAATATTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT 1921 	1922 TITICTAAACACAAIIGITATAGCCAGAGGAACAAAGAIGGATATAAAAITATTGTTGCC 1981 	1982 CTGGACAAAATACATGTATWTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA 2041 	2042 TITTAAAAAACCIGAATIGGGAANGGAANTIGGTAAGGTIGGCCAAANCTITTIGAAAA 2101 2259 TITTAAAAACIGAATTGGAATAGAATIGGTAAGITGCAAAGACTITIGAAA 2312	2102 TAATTAA 2108 2313 TAATTAA 2319	RESULT 3 AR222022 LOCUS AR222022 2825 bp DNA linear PAT 20-DEC-2002	TITON Sequence 1 from patent US 6455283. SION AR232022. N AR232022.1 GI:27273902 ADS		AUTHORS Ferrara, N. and Kuo, S.S. TITLE Nucleic acids encoding vascular endothelial cell growth factor-E	JOURNAL Patent: US 6455283-A 1 24-SEP-2002; PEATURES Location/Qualifiers	

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Hillan,K.J., Kuo,S.S., Tumas,D. and Wood,W.I.
Compositions and methods for the treatment of immune related
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          122 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA 181
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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/organism="Homo sapiens"
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          TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGCACACAGGAGATAGCCGCATC 1081
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                                                                                        1682 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGATAAACCTGAAAAGAAGAGTGG 1741
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Promotion or inhibition of angiogenesis and cardiovascularization Patent: Wo 0073445-A 3 07-DEC-2000;
Genentech Inc. (US)
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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93.9%; Score 1979.4; DB 6; Length 2849;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps
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/organism="Homo sapiens"
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1630 GITCHGIATITCAGITCITTCGAIACGGCITAGGGIAATGICAGIACAGGAAAAAAACTG 1689
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                                                                 970 TIGGAAGAAAAICCAGAGIGGIGGAICIGAACCIICIAACAGAGGAGGIAAGAITAIACA 1029
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                                 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA
                                                                                                    GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA
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517 TGACATCTGCCCTGGCCGGCCAGAGACAGGGACTCCAGGCGGAATCCAACCTGAGTAGTA 576
                                                                                                                                                                                                                                        TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 241
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                                                                            AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181
                                                                                                                                                                                                                                                                                                                                                                                                GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301
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                                1657 TTACAGTGCATTCTGAAAGAGAGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1716
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                                                                          TTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
                                                                                                                                                                        1777 TTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1836
                                                                                                                                                                                                         GTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTG 1896
                                                                                                                                                                                                                                                                      TGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTGCATGTCCTGGGCCT 1501
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                 1202 TTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT
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/evidence=not_experimental
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ICKYDFVEVEREPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY
NIVMPQFTEAVSPSYLPPSALPLDLANAITPRSTLEDLIRILBFERWQLDLEDLYRP
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VKRCGGRACACCLHNCNECQCVPSKVTKKXHEVLQLRFRTGVRGLHKSLTDVALEHHEE
CDCVCRGSTGG"
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
1 (Dases 1 to 3007)
1 Tasi, Y.J., Lee, R.K., Lin, S.P. and Chen, Y.H.
1 Identification of a novel platelet-derived growth factor-like gene, fallotein, in the human reproductive tract

Biochim. Biophys. Acta 1492 (1), 196-202 (2000)
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                                                                                                                                                                                                                                                                                                                                          Z (bases 1 to 3007)
Tsai, Y.J., Lee, R.K.K. and Lin, S.P.
Direct Submission
Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial
Bospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan
Location/Qualifiers
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492. .1529
/note="found in female reproductive tract"
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Db 1957 AAAACCGAFTATTTTTTTTTTTTTTTTTTTTTTTTTTTTT	RESULF 9 AX739931 LOCUG AX739931 LOCUG AX739931 AX718; AX7001906 AX801N AX718; AX7001906 AX70
422 TACCAGGAAACCAATTCTAAAGGAAATCAAATTAGGATAAGATTGTATCTGATGAAT 481	

2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAATGAGCCTCTTCGGGCTTCTCCTGG 61 128 CCCGCGTGAGTGAGCTCTCACCCCAGTCAGCCAATGAGCCTCTTCGGGCTTCTCTCTGC 187 62 TGACATCTGCCCTGGCCGAGAGCGAGAGCGAGCGCGAATCCAACCTGAGTGA 121 188 TGACATCTGCCCTGGCCGCCAGAGACGAGACTCAGCGGAATCCAACCTGAGTAGTA 121 122 AATTCCAGTTTCCAGCAACAAGAACGGACTACAAGATCCTCAGCATAGTA 247 122 AATTCCAGTTTCCAGCAACAAGAACGGAGTACAAGATCCTCAGCATGAGAA 181 248 AATTCCAGTTTTCCAGCAACAAGAACGGAGTACAAGATCCTCAGCATGAGAAA 307	182 TTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATCCAA 241 308 TTATTACTGTGTTACTAATGGAAGTATTCACAGGCCAAGGTTTCCTCATACTTATCCAA 367 242 GAATACGGTCTTGGTATGGAGATTAGTAGGAGAAAATGTATGAACTTA 301 368 GAATACGGTCTTGGTATGGAGATTAGTAGAGGAAAAATGTAGAATTA 427	02 CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG 3 [22 TACCAGGAAACAGATTICTAAAGGAAATCAAATTAGGATAAGATTIGTATCTGATGAAT 48 18 TACHHIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIIII	42 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATAATAATAATAATAATAATAATAATAATAATA	CATTACTACTACTACTACTTCGAAGACCTTATTCGATATCTTGAACCAGAGAGAG	722 TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGGGTAAGATTATACA 781 [11]	42 ITTI 68 ITTI 02 ACAP 28 ACAA	962 TTCAGTTGAGACCAAGACCGGTGTCAGGGGATTGCACAAATCACTCCCCGCGTGGCCC 1021 1088 TTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCAC
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1502 AAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTTGCTCATATTCACATATGTAAAC 1560
1628 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAAAC 1687
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Homo sapiens platelet-derived growth factor C (PDGFC) mRNA,
complete cds.
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                                                                                    Elkaryoza, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1804)

2 (albertson, D.G., Duff, M.E., West, J.W., Kelly, J.D., Sheppard, P.O., Hofstrand, P.D., Gao, Z., Shoemaker, K., Bukowski, T.R., Moore, M., Feldhaus, A.L., Humes, J.M., Palmer, T.E. and Hart, C.E. Platelet-derived growth factor C (PDGF-C), a novel growth factor J. Binds to PDGF alpha and beta receptor J. Binds to PDGF alpha and beta receptor J. Biol. Chem. 276 (29), 27406-27414 (2001)
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Gao,Z., Hart,C., Piddington,C., Sheppard,P., Shoemaker,K.,
Gilbertson,D., West,J. and O'Hara,P.J.

Direct Submission
Submitted (26-APR-2000) Biomolecular Informatics, ZymoGenetics,
Inc., 1201 Eastlake Avenue East, Seattle, WA 98102, USA
Location/Qualifiers
                                                                  1142 AIGCGITAICTCCAICCITAAICTCAGTIGITIGCTICAAGGACCTITCATCAICAGAI
                                                                                                                                 1202 TTACAGTGCATTCTGAAAGAAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT
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                                                                                          TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGCACAGGAGGATAGCCGCATC
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                                                                                                                      ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC
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from patent US 6495668.
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/db xref="GI:14009504"
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VKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEE
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1. .1804
                                                                   /note="PDGF-C;
                                    /gene="PDGFC"
163. .1200
/gene="PDGFC"
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Best Local Similarity
Matches 1639; Conserv
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  Unknown to 1760)

1 (bases 1 to 1760)

2 (bases 1 to 1760)

Glibert, T., Hart, C.E., Sheppard, P.O. Growth factor homolog ZVEGF4

Patent: US 6495668-A 32 17-DEC-2002;

Location/Qualifiers
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                                                    /organism="unknown"
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(ao, X., Hart, C.E., Piddington, C.S., Sh Gilbertson, D.G. and West, J.W.
Growth factor homolog zvegf3
Patent: US 6528050-A 1 04-WAR-2003;
Location/Qualifiers
1.1760 AR282949 1700 patent US 6528050. AR282949 GI:29719770

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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                               TGGAGCACCATGAGGAGTGTGACTGTCTGCAGAGGGAGCACAGGAGGATGATC
                                                                  Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G. Growth factor homolog zvegf4
Patent: WO 0066736-A 32 09-NOV-2000;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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/protein_id="CAC17170.1"
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AX044518.1 GI:11343373
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Mammalia; Eutheria; Primates, Catarrhini, Hominidae, Homo.
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Patent: WO 0128586-A 1 26-APR-2001;
ZymoGenetics, Inc. (US)
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                     Direct Submission.

Submitted (12-07-1999) Tsuyoshi Hamada, Nippon Medical School, Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo 113-8602, Japan (E-mail:t-hamada@nms.ac.jp, Tel:s1-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

Tel:s1-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

Tel:s1-3-3822-2131(ex.5277), Fax:81-3-5814-1684)

I. Organism="Homo sapiens"

Ab xref="taxon:9606"

/tissue type="mkN"
/db xref="taxon:9606"

/tissue type="hrain"
/dc xref="taxon:9606"

I. J817

I. 317

Sgene="hSCDGF"

Sgene="hSCDGF"

Codon statt=1

/codon statt=1
/roduct="spinal cord-derived growth factor"
/hrotein id="spinal cord-derived growth factor"
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0; Mismatches 13;
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Hamada,T., Ui-Tei,K. and Miyata,Y.

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Hamada,T., Ui-Tei,K. and Miyata,Y.
Direct Submission
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| SIDSI / gogdata/geneseq/geneseqn-embl/NA1995.DAT:*
| SIDSI / gogdata/geneseq/geneseqn-embl/NA1996.DAT:*
| SIDSI / gogdata/geneseq/geneseqn-embl/NA1997.DAT:*
| SIDSI / gogdata/geneseq/geneseqn-embl/NA1999.DAT:*
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2108
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                 Run on:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	cDNA encoding plat	Human VEGF-E DNA.	DNA encoding human	Human TANGO 128 co	Human PRO200 nucle	Human PRO200 (UNQ1	Human PRO200 (VEGF	Human PRO200 prote
QI	AAA12523	AAZ23691	ABS57294	AAA47452	AAZ34296	AAC78582	AAA88515	AAC58579
80	21	50	25	21	20	21	7	21
% Query ore Match Length DB II	2108	2825	2825	2839	2849	2849	2849	2849
% Query Match	8.66	93.9	93.9	93.9	93.9	93.9	93.9	93.9
SCC	2103.6	1979.4	1979.4	1979.4	1979.4	1979:4	1979.4	1979.4
Result No.	н	73	m	4	ß	9	7	∞

Human PRO713 cDNA	CDNA S	PR0200	PRO200 codi	Human anglogenesis	cDNA encoding huma	Human cDNA encodin	DNA encoding novel	cDNA encoding huma		Human RACE generat	cDNA encoding huma	Bone morphogenic p	vascula	VEGF-X	Human VEGF-X homol	Human LP8, a PDGF-	Human platelet-der	ncodin		norphoge	Human zvegf3 DNA,	Human growth facto	Human Zvegf3 DNA.	Human cDNA encodin	Human zvegf3 codin	hum	encoding a		VEGF/P	VEGF-X	VEGF-X	VEGF-X	VEGF-X	A X	VEGF3 fu	Human zvegf 3/malt
AAA77621	AAS21386	AAC90564	AAC88962	Ó	ACA03745	ACA04166	ABX89283	ABX92668	AAS12884	AAA71951	AAA52458	AAZ48599	ABQ81461	AAA71990	AAA71952	AAD06812	AAC64426	AAX86352	AAF18314	AAZ48600	AAC81582	AAA51498	AAD04649	ABS68612	AAI72443	ABX93146		AAF82259	ABN88974	AAA71955	AAA71936	AAA71982		æ	2	ABS68655
21	22	22	22	22	25	25	25	25	22	21	21	21	24	21	21	22	21	20	21	21	21	21	22	24	24	25	21	22	24	21	21	21	21	21	21	24
2849	2849	2849	2849	2849	2849	2849	2849	2849	3007	2475	2779	2858	2632	2668	2776	2827	2896	2898	3087	2794	1760	1760	1760	1760	1760	1760	1536	1328	1328	1473	1878	1716	13	1710	1095	1095
93.9	93.9	93.9	93.9	93.9	93.9	93.9	93.9	93.9	93.9	93.8	93.8	93.8	93.4	93.4	93.2	93.1	93.1	93.1	90.5	88.4	77.1			77.1			72.7									47.2
1979.4	1979.4	1979.4	1979.4	1979.4	1979.4	1979.4	1979.4	1979.4	1979.4	1977.8	1977.8	1977.8	1968.4	1968.4	1965.2	1962.6	1962.6	1962.6	1908	1863.8	1624.8	_:		-	1624.8		1532.2							1018	4.	94.
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ALIGNMENTS

AAA12523 standard; cDNA; 2108 BP.

RESULT 1

AAA12523

AAA12523;

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Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling; ss.
                                                                                                                                                                                Location/Qualifiers
37-1073
7-tag = a
/product = "platelet-derived growth factor C"
                                                         CDNA encoding platelet-derived growth factor C (PDGF-C).
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98US-0108109
                                  25-JUL-2000 (first entry)
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                                                                                                                                                          Homo sapiens
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12-NOV-1998;
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GTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGGCGCTGGTGTGGTTCTGGTACT 420
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                                                             TATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATGTCATGCCACAATTCACA
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                                                                                                                                                                         Uutela M,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 99.8%; Score 2103.6; Best Local Similarity 100.0%; Pred. No. 0; Matches 2108; Conservative 0; Mismatches
                                                                                                                                                                         Lee X, Ponten A,
Betsholz C;
                                                                                                        LUDWIG INST CANCER RES.
UNIV HELSINKI LICENSING LTD.
                                                                                                                                                                                                                                                                                                                                                                                          Claim 9; Fig 1; 135pp; English.
                    98US-0113002.
99US-0135426.
99US-0144022.
                                                                                                                                                                         Aase K,
Heldin C,
                                                                                                                                                                                                                                    WPI; 2000-292954/25.
P-PSDB; AAY84557.
                                                                                                                                                                                            Heldin
                                                                 15-JUL-1999;
    03-DEC-1998;
18-DEC-1998;
                                                                                                                                                                         Eriksson U,
                                                                                                                                                                                                Oestman A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61
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This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VBGF-E) polypeptide which has tranquillizer, vulnery and cardiant activity. VBGF-E can be administered therapeutically, especially by expressing encoding polymucleotides, to treat cardiovascular or endothelial disorders in mammals, especially the wastern and may especially by expressing encoding polymucleotides, to treat cardiovascular or endothelial disorders in mammals, especially cregeneration, and may especially be used to treat cardiac hypertrophy or tream to treat cardiac hypertrophy or tream to treat cardiac hypertrophy or treat angiogenic disorders in mammals (especially humans) e.g. cancer or screen for antagonists and agonists, and the antagonists administered to treat angiogenic disorders in mammals (especially humans) e.g. cancer or age-related macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation), by contacting the antibody with a tissue sample and detecting formation of an antibody varger bolypeptide complex. Polypuclecides encoding (VBGF-E can be used to diagnose cardiovascular, and encoding to the wastern as angles. They can also be used to diagnose a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, endothelial or angiogenic disorder such as a tumor), by cardiovascular, on the VBGF-E encoding sequence from of effecting a mutation in the VBGF-E encoding sequence is solated from a sample. They may also be used to probes useful to detect related as an encoding sequences or for gene mapping. This sequence encodes the human VBGF-E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TGACATCTGCCCTGGCCGGCCAGACGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequences or for gene mapping. This sequence encodes the human VEGF-E protein described in the method of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCCTGC
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                                                                                                                                                                                                                                                                                                                                                                      New growth factor polypeptide useful for treating cardiovascular or endothelial disorders, e.g. cardiac hypertrophy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 20; Length 2825;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1979.4; Pred. No. 0; 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 2; Fig 1; 122pp; English.
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Best Local Similarity 97.7%;
Matches 2059; Conservative
                                                         98US-0040220.
98US-0184216.
99WO-US05190
                                                                                                                                                      (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                            WPI; 1999-580306/49
                                                                                                                                                                                                                                                                                                            P-PSDB; AAY33679
                                                                                                                                                                                                                   Kno
   10-MAR-1999;
                                                            17-MAR-1998;
                                                                                            02-NOV-1998;
                                                                                                                                                                                                                   Ferrara N,
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                                                                      1501 TAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAAAC
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                                   TAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTGCTCATATTCACATATGTAAAC
                                                                                                                                                                                                            1561 CAGAACATTCTATGTACTACAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTA
                                                                                                                                                                                                                                                                                                                                      AACTIGIGICKIGCIGATAGGACAGACIGGATITITICATATITICATATITIAAATITICIGC
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                                                                                                                                                      CAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTA
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259..1296
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/product= "VEGF-E"
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                                                                                                                                                                                       Nucleic acids encoding TANGO polypeptides are useful as modulating agents for regulating cellular processes like asthma, graft versus-host diseases, rheumatoid arthritis, postriasis, inflammatory bowel disease, septic shock, ulcerative colitis, Crohn's disease, chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, cancer, liver disease, Hodgkin's chronic myelogenous leukemia, qualitation diseases e.g. myasthemia gravis, autoimmune diabetes and systemic lupus erythematosus. The nucleic acids are also useful for producing transgenic animals and the TANGO polypeptides themselves. Partial TANGO-128, 140, 197, 212, 213, 224, 239 sequences are useful in forensic biology, for diagnostic assays, prognostic assays, pharmacogenomics and for monitoring clinical trials. TANGO polypeptides are suitable for both prophylactic and therapeutic methods for treating a subject at risk of a disorder or having a disorder associated with aberrant TANGO expression. A wide range of cellular disorders can be treated.
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Novel nucleic acid sequences encoding TANGO-128, 140, 197, 212, 213, 224 and 239 polypeptides useful for the treatment of asthma, rheumatoid arthritis, psoriasis and autoimmune diseases
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1; Mismatches
                                                                                                                                   Claim 1; Fig 1; 209pp; English
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Best Local Similarity 97.7
Matches 2059; Conservative
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PR 27-MAR-1998; 98US-0079528.

PR 37-MAR-1998; 98US-0079920.

PR 37-MAR-1998; 98US-0079920.

PR 37-MAR-1998; 98US-0079920.

PR 31-MAR-1998; 98US-0079923.

PR 31-MAR-1998; 98US-0080105.

PR 31-MAR-1998; 98US-0080107.

PR 01-APR-1998; 98US-0080107.

PR 01-APR-1998; 98US-00801195.

PR 01-APR-1998; 98US-00801195.

PR 01-APR-1998; 98US-00801195.

PR 01-APR-1998; 98US-0081195.

PR 01-APR-1998; 98US-0081521.

PR 01-APR-1998; 98US-0085581.

PR 01-APR-1998; 98US-008558
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Query Match
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps

Oy 2 CCCCCCTCACCCCCAGTCACCACTTCCCGCTTCCCGGCTTCTCCCTGG 61

62 TGACATCTGCCCTGGCCGGCCAGAGACGAGGGACTCCAGGCGGAATCCAACCTGAGTAGTA 121

CCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGC

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us-09-852-209a-2.rng

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AAC7845B to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polypeptides. The PRO polynucleotides and polypeptides have cytostatic activity. The polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bloactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting the polypeptide for specific targeting. The polypeptide targeting the polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78877 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                          Novel PRO polypeptides and polynucleotides used in detection methods, to target bioactive molecules to specific cells, and to modulate cellular activities -
Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL, Ferrara N, Filvaroff E, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A, Godoweki PJ, Grimaldi CJ, Gurney AL, Hillan KJ, Kliavin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA, Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                            Claim 2; Fig 206; 636pp; English.
                                                                                                                                                         WPI; 2000-611443/58.
P-PSDB; AAB44322.
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Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

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5	61	121	369	181	429	241	489	301	549	361	609	421	699	481	729	541	789	601	849
Gaps	CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG	CTGGCCGGCCAGAGGAGGAGTCAGGCGAATCCAAACCTGAGTAATA		AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATGAGAAAAAAAA	AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGGAA	CCAA	TTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCAAGGTTTCCTCATACTTATCCAA	GAAATACGGTCTTGGTATGGAGATTAGCAGTAGAGGAAAATGTATGGATACAACTTA	GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA	CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG	CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTTTTTG	TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCGCTGGTGGTTCTGGTACTG	TAGAAGTTGAGGAACCCAGTGATGGAACTAATATAGGGCGCTGGTGGTGGTTCTGGTACTA	TACCAGGAAAACGGATTTCTAAAGGAAAATCAAATTAGGATAAGATTTGTATCTGATGAAT	TACCAGGAAAACAGATTICTAAAGGAAATCAAATTAGGATAAGATTIGTATCTGATGAAT	ATTITCCTTCTGAACCAGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG	ATTICCTICIONALONG	AAAGCIGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG	AAGCIGIGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG
	orici	SAGT	SAGT	IGAG	TGAG	TTAT	TTAT	ACAA	ACA.	TGAT	TGAT	IGGI	IGGI	IGAT	IGAT	ATTC	ATTC	TAAT	TAAT
11;		ACCT.	_ğ_	GCA	GCA.	ATAC	ATAC	3GAT	GAT	GTA.	GTA	STIC	STTC.	PATC	CATC	ACA	- ACA	GCT.	-67-
Length dels	1 - F	CCA		CTC 	CTC	CTC	CTC	TAT	TAT	GCA	-GC-	GTG	-5 -5	TTG	-11 -11 -12	TGC	TGC	ACC	POC.
		GAAT	GAAT	GATC	GATC	TACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTAT	TTT	AATG	AATG	ATAT	ATAT	1661	1661	AGAT	AGAT	GTCA	GTC	OTTG	-00
B 21;	GAGC	9999		ACAA	ACAA	AAGG	AAGG	GGAA	GGAA	TGAC	TGAC	0500	-00 -00 -00	GATA	GATA	CATT	CAL	6000 	- 50 - 50 - 50 - 50
DB 36	TAAA	CTCA		SAGT	GAGT	2005	2005	TAGA	raga	AAGA	AAGA	TAGG	TAGG	TTAG	TTAG	ACAA	ACAA	CTTT	CTTT
0.4; 0; ches	20-10 	3GGA	- AG-	AACG	AACG.	CACA	ZACA.	SCAG	SCAG.	CCAG	CAG	TAT	TAT	AAA	AAA.	CACT	SACT.	FCAG	CAG
1979 No. (GTC	ICGA(CAG	CAG	CAG	PATT	ATT	GTA(GTA	GAC	GAC	A CT	ACT.	AAT	AAT	ATC	ATC	CCT	CCT
Score 1979.4; Pred. No. 0; ; Mismatches	1000 	GAG	GAG	GGA	GGA	AAG	AAG	ATT	ATT	TGA	TGA	TGG	TGG	AGG2	- 60 - 60 - 60 - 60	STO-	-crg	ACC	ACC
Sc Pr	TCAC	200		ACAA	ACA	ATG	ATGG	GGAG	GGAG	GGC1	-86 -72	GTGA	Gra	CTAB	CTA	GGTT	GGTT	1367	TGCT
93.9%; 97.7%; ive	SCTC 	5000		AGCA	AGCA -	ACTA	ACTA	TATE	STAT	TTTG	TTT	CCCA	CCC	ATTT	ATTT	CCAG	CCAG	TCAG	TCAG
93 97 It ive	TGA 	S CT	_P.	11CC	-0 -0 -1:	TUE	FICT.	ATT.	-1: -0:	AGA	AGA.	GAA	-SEA	CAG	CAG	GAA	GAA	100 	CC
ty	TGAC	TGACATCTGCC		GTTI	GTTJ	TGTC	TGT	GGTC	GGTC	TGA	TGA	TGAC	TGAC	AAAA	AAA	TTC	- L	GAG	GAG
lari Cons	0000	CATO	CATC	TCCA	ICCA	TTAC	TTAC	ATAC	ATAC	TTGA	TTGA	AAGT	AAGI	CAGG	-05 -05 -05 -05	TTCC	TICC	CTGI	Cre
Similarity 97.79; Conservative				AAT	AAT.	TTA		GAA	GAA	CGT	-G-	TAG		TAC	-	ATT	•		•
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Ši i	0 1	CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 661
a 6	u v	AACTGCCTTTAGTACCTTGGAAGACCTTATCGATATCTTGAACCAGAGATGGC 50
중 음	910	AGITGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTGGCAAGGCTTTTGTT 721 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTT 969
ò	~	ABGAAAATCCAGAGTGGGTCTGAACCTTCTAACAGAGGGGGTAAGATTATACA 781
d d	970	TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATATACA 1029
δ	ö	
qq	m	GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGAAGAACTAAAGAGAACCGATACCA 1089
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g		TTTTCTGGCCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAAACTGTGCCTGTTGTCTCC 1149
λ t	902	ACATTGCAATGAATGTCAATGTCTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 961
3	n ·	
중 음	962	TTCAGTTGAGACCAAAGACCGGTGTTGAGGGGATTGCACAAATCACTCAC
ò	1022	TGGAGCACCATGAGGAGTGTGTGTGTGCAGAGGAGCACAGGAGGATAGCCGCATC 1081
DP	~	
λŏ	1082	ACCACCAGCACTCTTGCCCAGAGCTGTGCAGTGCAGTGGATTCTATTAGAGAACGT 1141
QQ	1330	ACCACCAGCAGCTCTTGCCCCAGAGCTGTGCCAGTGGCTGATTCTATTAGAGAACGT 1389
ķ	1142	
Dp	1390	
ò	1202	TTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261
Db	1450	
ò	1262	TTGRGAGGGGGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAA
qa	1510	
ζ		TTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
Dþ	1570	
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Q O	m	GTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTG 1689
č	1442	TGCAAGTGAGCACCTGATTCCGTTGCCTTAAACTCTAAAGCTCCATGTCCTGGGCCT 1501
qq	1690	TGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1749
ζŏ	1502	AAAAICGIAIAAAAICIGGAITITITITITITITITITIGAAAITCACAIAIGIAAACC 1561
DÞ	1750	ਜ
à	1562	162
qa	1810	7
ò	1622	7
Dβ	1870	192
δλ	1682	ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1741

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The present sequence is that of cDNA clone DNA29101-1272 or UNQ174 (ATCC 20963) isolated from a human glioma cell line G61 cDNA library using probes (see AAA88522-26) based on an expressed sequence tag (see AAA88522) identified on the basis of homology to vascular endothelial growth factor (VEGF). The clone contains a single open reading frame encoding a 345-amino acid protein (see AAB19578) comparing frame encoding a 345-amino acid protein (see AAB19578) comparing frame encoding a 345-amino acid protein (see AAB19578) comparing trame encoding a 345-amino acid protein (see AAB19578) comparing trame encoding a 345-amino acid protein (see AAB19578) comparing trame encoding a 345-amino acid protein (see AAB19578) comparing the comparing production of PRO200 (VEGF-E). The invention relates to the use of PRO polypeptides, including PRO200, to delay, prevent or rescue retinal cells displaced retinal ganglion cells, displaced retinal ganglion cells, displaced macrine cells, displaced retinal ganglion cells, amacrine cells, displaced macrine cells, including Mueller cells and bipolar neurons, and supportive cells (including Mueller cells and bipolar neurons, and supportive cells (including Mueller cells and bipolar neurons, and supportive cells (including Mueller cells and coular disease selected from retinitis pigmentosa, macular cells are preferably photoreceptors and photoreceptors and photoreceptors of degeneration, including age-related, retinal detachment, retinal cells, telmopathy, retinal degenerative myopia, acute retinal neurosis syndrome, traumatic chorioretinopathies or conditions such as central or branch retinal vision coclusion, collagen vascular diseases, thrombocytopenic purpura, cedema, ischinal vasculitis and occlusion associated with Eales and systemic lupus erythematosus (claimed).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     250 cccdccchcachcacchchccccachcaccaancaccrchrcccccrcrrccrccrcc 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  310 TGACATCTGCCCTGGCCGGCCAGAGACACAGGGGAATCCGAATCCAACCTGAGTA 369
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             370 AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA 429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 241
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG 361
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 729
                                                                             Novel PRO polypeptides useful for preventing or rescuing retinal cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCCAAATGAGCCTCTTCGGGCTTCTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   11; Gaps
                                                                                                 from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 1979.4; DB 21; Length 2849;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. 0;
                                                                                                                                                                                                               Example 8; Fig 1; 140pp; English.
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97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity 97.7
Matches 2059; Conservative
  WPI; 2000-587437/55.
                               P-PSDB; AAB19578.
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                                                                                CCTIAICTICACTITAICGAIAAGICAGITIAITIGITITCAITGIGIACAITITIAIAIT 1801
                                                                                                                                                                                           TTTTAAAAACCTGAATTGGGAANGGAANTTGGTAAGGTTGGCCAAANCTTTTTTGAAAA 2101
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                                                                                                                                                                                                                             CTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTTTTTTACC
                                                                                                                                                                                                                                                                                                                                                         AAAGGIATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2227 TCTGACAAAAATACATGTATTT-CATTCTGTATGGTGCTAGAGTTAGATT-AATCTGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1982 CTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA
                                                                                                                                                                                                                                                                                               AAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT
                                                                                                                                                                                                                                                                                                                                                                                                             TITICIAAACACAATIGITATAGCCAGAGGAACAAAGAIGGATAIAAAAAATATIGITGCC
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ocular disease; retinopathy; maculopathy; therapy; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; macular hole; myopia; traumatic chorioretinopathy; acute retinal necrosis syndrome; contusion; edema; retinal vision occlusion; vascular disease; retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO200; vascular epithelial growth factor E; VEGF-E; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human PRO200 (VEGF-E) cDNA clone DNA29101-1272
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hebert C,
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Kuo SS, La Fleur M,
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285..1322
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AAC58579 standard; cDNA; 2849 BP
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     730 ATTITCCTICIGAACCAGGGTTCTGCATCCACTACAACATGTCATGCCACAATTCACAG
                                                        AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT
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                                           AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG
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Marmatological; antiarthritic; antirhaumatic; immunosuppressive;

Machaeostalic; antiathyroid; antidabetic; nootropic; neuroprotective;

W antianaemic; hepatotropic; virudide; antipsoriatic; antiallargic;

antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;

M osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;

W diopathic inflammatory myopathy; systemic sclerosis; sarcoidosis;

W systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;

W autoimmune thrombocytopaenia; immune-mediated franal disease;

Inflammatory bowel disease; pluten-sensitive enteropathy;

M untoimmune disease; immune-mediated skin disease;

M untoimmune disease; immune-mediated skin disease;

M untoimmune disease; immune-mediated skin disease;

M untoimmune disease; transplantation associated disease;

M graft rejection; graft-versus-host-disease; ss.
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AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621
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99WO-US28564.
99WO-US28565.
99WO-US30095.
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06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US03565.
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2000WO-US00219.
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                99US-0123957
                        99US-0125775.
                            99US-0128849
                                                            99WO-US12252
                                                                       99US-0144758
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                                   99WO-US08615
                                         99US-0131445
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                                         28-APR-1999;
04-MAY-1999;
14-MAY-1999;
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23-JUN-1999;
20-JUL-1999;
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                                   20-APR-1999;
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29-0CT-1999;
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                                                                                              08-SEP-1
13-SEP-1
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(GETH) GENENTECH INC.

Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W; Lu Y, Pan J, Pennica D, Shelton DL, Smith V; umas D, Watanabe CK, Wood WI, Yan M; Kabakoff RC, Lu Y, P. Stewart TA, Tumas D, Ashkenazi AJ,

WPI; 2000-572271/53. P-PSDB; AAB33414.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus

Claim 23; Fig 1; 309pp; English.

The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and diagnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, sjogram's systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombooytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, hepatobiliary diseases of the central and peripheral nervous systems, hepatobiliary diseases, inflammatory own peripheral nervous systems, hepatobiliary diseases, inflammatory of immune or immune-mediated skin diseases, allergic diseases, autoimmune or immune-mediated skin diseases, allergic diseases, incombing graft relection and graft-versus-host-disease.

Immunological diseases of the lung, and transplantation associated diseases including graft relection and graft-versus-host-disease.

AAC58377 to AAC58378 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAC58579 to AAC58422 and

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TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGAAGATATAAACA 1029
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AAB33414 to AAB33477 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention.
                                                                                         DB 21; Length 2849;
                                                                                                                             1; Mismatches 36; Indels
                                                       Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
                                                                                         Score 1979.4;
Pred. No. 0;
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Best Local Similarity 97.7%;
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TITIAAAAAACTGAATI--GGAATAGAATTGGTAAGTT---GCAAAGACTTTTTGAAAA 2338
                                                                                                                                                                                                                                        Human, PRO, promotion; inhibition; angiogenesis; cardiovascularisation; diagnosis; trauma, wound; cancer; atherosclerosis; cardiac hypertrophy; angiogenic; proliferative; cardiant; cardiovascular; antiatherosclerotic; cytostatic; gene therapy; vaccine; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovascularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovascular, endothelial or
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tuo SS, Paoni NF, Smith V;
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Klein RD,
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                                                                                                                                     standard; cDNA; 2849
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Gurney AL, Kl
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angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hymertrophy). For example, the nucleic acids (NCs) and vectors
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ස ර	902 A	902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 961
ò	962 7	TCAGTTGAGACCAAAAGACCGGTGTCAGGGGATTGCACAAATCACTCAC
qa	1210 T	<u>TCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCAC</u>
<i>දි</i> ර අය	1022 T	GGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAGCACAGGAGGATAGCCGCATC 1081
λ'n	1082 A	CCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGGTGGTTGTTTTATTAGAGAACGT 1141
Ор	1330 A	
à :	1142 A	INCOTTATCTCCATCATAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1201
gg	1390 A	INGCGTTATCTCCATCCTTAALCTCAGTTGTTGCTTCAAGGACCTTTCAGGAT 1442
සි ර	1202 T	TACAGTGCATTCTGAAAGAGAGAGACTTCTGAAATTAGGATTGTCAAAGGTTT 1201
È	1262 1	TGAGAGGGGGGTAAAGGACAGGAGAAAAGGCTTTCAATCGTGGAAAGAAA
ф	1510 j	tgagaggaggcctaaaggacaggagaaaaggtcttcaatcgtggaaagaaa
& &	1322 1	TGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
à	1382	FITCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTG 1441
d d	1630	
ò	1442 7	GCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1501
qq	1690 1	GCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1749
ò	1502	NABATICITATABABITITITITITITITITITITITICICATATITICACATATATACC 1561
qq	1750 7	AAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTTTT
à	1562 7	AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621
QQ	1810 }	sgaacatictatgtactacaaacciggtrifitaaaaagaactatgtigctatgattaa 1869
λ	1622 #	ACTIGICATCRIGCIGATAGGACAGACTGGATTITTCATATITCTTATTAAAATTICTGCC 1681
අු	1870 7	ACTTGTGTCATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAATTTCTGCC 1929
රු අ	1682 7	atttagaagaagaactacattcatggtttggaagagataaacctgaaaagaagagtgg 1741
č	1742 (CTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATT 1801
q _O	1990	
õ	1802 (TICCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTATTTTTACC 1861
qq	2050	
ò	1862 /	AAAGGTATTTAATATTCTTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT 1921
qq	2110	aadgotattitaatattettittittatgacaacttagatcaactattettagettiggtaaat 2169
ζ	1922	ITITCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGTAGAAAAATATTGTTGC 1981
අධ	2170	ITTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGATATAAAATATTGTTGC 2226
λŏ	1982 (CTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA 2041

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2227 TCTGACAAAATACATGTATTT-CATTCTCGTATGGTGCTAGAGTTAGATT-AATCTGCA 2284
                                             TITIAAAAAACTGAATT---GGAATAGAATIGGTAAGTI---GCAAAGACTTTTTGAAAA 2338
                                                                                                                                                                                                  Human secretory and transmembrane; PRO; mammalian; cancer; lung; breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
4E, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
                           TITITAAAAACCTGAATTGGGAANGGAANTTGGTAAGGTTGGCCAAANCTTTTTTGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isolated, secretory and transmembrane PRO polypeptide used to detect
                                                                                                                                                                                    Human cDNA sequence encoding for PRO200 polypeptide.
                                                                                                                              AAS21386 standard; cDNA; 2849 BP.
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01-MAR-2000; 2000MO-USOS501.

21-MAR-2000; 2000MO-USO7537.

21-MAR-2000; 2000MO-USO7532.

30-MAR-2000; 2000MO-USO8439.

17-MAY-2000; 2000MO-USI1404.

30-MAY-2000; 2000MO-USI4941.

02-UJN-2000; 2000MO-USI5264.
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06-JAN-2000; 2
11-FEB-2000; 2
18-FEB-2000; 2
22-FEB-2000; 2
24-FEB-2000; 2
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09-DEC-1999;
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AASIJISIA -AASIJISIA encode tor novel numen secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to medulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TMF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation of chondrocytes, the proliferation of a cytokine from peripheral blood of T-lymphocytes, the release of a cytokine from peripheral blood the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide coffactor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             489
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Gaps
other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. lung, breast, prostate, cervical
                                                                                                                                                                                                                                                                                           AAS21244-AAS21518 encode for novel human secretory and transmembrane
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 1979.4; DB 22; Length 2849;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches
                                                                                                                                                                                                         Claim 3; Fig 285; 813pp; English.
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δ	602 CIARAACHGCCTTAGAACACCTTATTCGAACATATCTTGAACCAGAGAGATGGC 661	 DD 1930 ATTTAGAAG	ATTTAGAAGAAGAACTACATTCATGGTTTGG
qu	850 CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGGAGGC 909	Oy 1742 CCTTATCT7	TCACTTTATCGATAAGTCAGTTTAT
λō	662 AGTIGGACTIAGAAGAICIAIAIAGGCAACTICGCAACTICTIGGCAAGGCTITIGITT 721	1990	CTTATCTTCACTTTATCGATAAGTCAGTTTAT
ପ୍ପ	910 AGTIGGACTIAGAAGAICTAIAIAGGCCAACTIGGCAACTICTIGGCAAGGCTITIGTTI 969	1802 0	PGACATTATAACTGTTGGCTTTTCTA
λō	722 TIGGAAGAAATCCAGAGIGGIGGIGGTCIGAACCTICIAACAGAGGIAAGAITATACA 781	2050	
q	970 TIGGAAGAAARTCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 1029	2002	TTAATATTCTTTTTATGACAACTT
ò	782 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841	2110	AAAGGTATTTAATATTCTTTTTATGACAACTTV
qa	1030 GCTGCACACCTCGTAACTTCTCAGATGTCCATAAGGGAAGAACTAAAGAAACCGATACCA 1089	1922	ACACAATTGTTATAGCCAGAGGAAC
δλ	842 TITICIGGCCAGGITGICICCIGGITAAAGCIGIGGGAACIGIGCCTGITGICIC 901	2170	
ପ୍	1090 TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGTGG	Qy 1982 CTGGACAA	aaaatacatgtatntccatcccggaa
δλ	902 ACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 961	2227	TCTGACAAAATACATGTATTT-CATTCTCGTA
qa	1150 ACARTHGCAATGAATGTCAATGTGTCCCAAGCAAGTTACTAAAAAATACCACGAGGTCC 1209	OV 2042 TTTTABABA	AAACCTGAATTGGGAANGGAANTTGG
λŏ	TTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTACCGCGGGGGGTG102	2285	
qa	1210 ITCAGIIGAGACCAAAAGACCGGIGICAGGGGAIIGCACAAAAICACICAC	Qy 2102 TAATTAA	2108
δλ O	1022 TGGAGCACCATGAGGAGTGTGAGAGTGTGTGTGAGAGGAGCACAGGAGGAGGATAGCCGCATC 1081	TA 	2345
ò	ACCACCAGCAGCTCTTGCCCCAGAGCTGTGCAGTGGCTGGTTCTATTAGAGAACGT	RESULT 11	
: 43 _		3061 A	i; cDNA; 2849 BP.
ò	1142 AIGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1201	AC AAC90564;	
ପ୍ଧ	1390 AIGCGITAICICCAICCTTAAICTCAGTIGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1449	XX DT 21-MAR-2001 (firs	rst entry)
ò	1202 TTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261	DE Human PRO200 cDNA	. T
ପ୍ର			iant; antiangiogenic; anti
Oy D	1262 ITGAGAGGGGCCTAAAGGACAGGAGAAAAGGTCTTCAAFCGTGGAAAGAAAATTAAATG 1321 	KW endothelial disor KW wound healing; ss	vulnerary; antianginal; gene therapy; card, endothelial disorder; angiogenic disorder; wound healing; ss.
ð	TTGTATTAAATAGATCACC		
7 da	TIGHTHINTAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTTCCACTAGCTGG	WO200	
δŏ	1382 GTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAACTG 1441	AX PD 07-DEC-2000.	
qa	1630 GITCIGIALITICAGITCITICGATACGGCITAGGGTAAIGTCAGTACAGGAAAAAAACIG 1689	17-MAY-2000;	2000WO-US13705.
ζ	1442 IGCAAGTGGGCACCTGATTCCGTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1501	02-JUN-1999;	9WO-US12252.
qu	1690 recangreaccaccreatrecerrecerrecerraaccreatecareceredecer 1749	20-JUL-1999;	90S-0141537. 90S-0144758. 90S-0145698
ò 6	1502 AAAATGGTATAAAATCTGGATTTTTTTTTTTTTTTTTGCTCATATTGACATATGTAAAGC 1561 1760 BABAATGGTATAAAATCTGGATTTTTTTTTTTTTGCTCATATTGAAAAGC 1561 1760 BABAATGGTATAAAAATGTAGAATTTTTTTTTTTTTTTT	28-JUL-1999; 01-SEP-1999;	990S-0146222. 99WO-US20111.
ò	AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 162	30-NOV-1999; 02-DEC-1999;	9WO-US28409.
q qq	AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAGGAACTATGTTGCTAGATTAA	16-DEC-1999; 11-FEB-2000;	9WO-US330095. 0WO-US03565.
λ0	1622 ACTTGTGTGTCRGCTGATAGGACGGACTGGATTTTTCATATTTCTTATTAAAATTTCTGC 1681	18-FEB-2000; 18-FEB-2000;	0WO-US04341. 0WO-US04342.
qq	1870 ACTIGICATGCTGATAGGACAGACTGGATTTTCATATTCTTATTAAAATTTCTGC 1929	24-FEB-2000; 02-MAR-2000;	2000WO-US05004. 2000WO-US05841. 2000WO-US05310
λo	1682 ATTTAGAAGAGAAGTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGGTGG 1741	15-MAR-2000;	0WO-US06884.

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AATCTTGTTAAATATGTCTATTTTTACC 1861
                                                                                                                                   ATTGTTTCATTGTGTACATTTTTATATT 1801
                                                                                                                                                                                                                                                                                    SGTAAGGTTGGCCAAANCTTTTTGAAAA 2101
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|GTAAGTT---GCAAAGACTTTTTGAAAA 2338
GAAGAGATAAACCTGAAAAGAAGAGTGG 1989
                                                                                                                                                                                    CAAAGATGGATATAAAAATATTGTTGC 1981
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|CAAAGATG---ATATAAATATTGTTGC 2226
                                                                                                                                                                                                                                    ATGGTGCTAGAGTTGGATTAAACCTGCA 2041
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tiarteriosclerotic; hypotensive; ; antiinflammatory; cytostatic; rdiovascular disease; r; cancer; periodontal disease;

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1090 TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAAACTGTGCCTGTTGTTCTCC 1149
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                                                                                                                                                                                                                                                                                                                                                                                                                      970 TTGGĄĄGĄĄĄĄTCCĄGĄGTGGTGGATCTGĄĄCCTTCTĄĄCĄGAGGAGGTĄAGATTATACA 1029
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                                                         790 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 849
AAGCIGIGAGICCIICAGIGCIACCCCCIICAGCIIIGCCACIGGACCIGCIIAAIAAIG 601
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                                                                                                                  CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC
                                                                                                                                                        910 AGTIGGACTIAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTITIGIIT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present sequence is one of seventeen nucleic acids encoding PRO polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or antigonists are useful for treating cardiovascular, endothelial or angiogenic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atheroscelerosis, hypertension, arterial restensors, Raymaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.
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                                                                                                                                                                                 Marsters SA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11; Gaps
                                                                                                                                                                                                                                                                                                                                                                   Seventeen nucleic acids encoding PRO polypeptides which are useful ir
diagnosis and treatment of cardiovascular, endothelial or angiogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 22; Length 2849;
                                                                                                                                                        Gerritsen ME;
                                                                                                                                              Ashkenazi AJ, Baker KP, Ferrara N, Gerber H, Gerritsen
Goddard A, Godowski PJ, Gurney AL, Kuo SS, Mark MR, Ma
Paoni NF, Pitti RM, Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
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Pred. No. 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 60; Fig 3; 182pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 93.9%;
Best Local Similarity 97.7%;
Matches 2059; Conservative
      21-MAR-2000; 2000WO-US07532.
30-MAR-2000; 2000WO-US08439.
                                                                                                                                                                                                                                                                                                                                                                                                                         disorders in a mammal -
                                                                                                  (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                          WPI; 2001-025251/03.
                                                                                                                                                                                                                                                                                                             P-PSDB; AAB50952
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                                                                                                               CTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGATAAATATATCTATTTTACC 1861
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          1870 ACTIGIGICALGCIGALAGGACAGACIGGALTITITCALATITICITATAAATTICIGCC 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compositions containing a PRO526, PRO719, PRO725, PRO1031 or PRO200 proteins for modulating immune response or proliferation of T-lymphocytes in mammal, especially for treating immune related disorders, e.g. graft rejection -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, PRO526; PRO719; PRO200; PRO725; PRO1031; immune related disease; inflammation; thyroiditis; demyelinating disease; skin disease; infectious disease; ss.
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                              1682 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG
                                                                         CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTTGTTTCATTGTGTACATTTTTATATT
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Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human PRO200 coding sequence
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Kuo SS,
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The present invention discloses the coding and protein sequences of human
                         proteins PRO526, PRO719, PRO725, PRO1031 and PRO200. These proteins, their coding sequences and antibodies can be used in the treatment of immune-related diseases, including systemic lupus erythematosus, rheumatoid arthritis, thyroiditis, immune-mediated renal disease, demyelinating diseases such as multiple sclerosis, hepatobiliary diseases including primary biliary cirrhosis, inflammarcry bowel diseases, including asthma, immuno-dogic diseases including asthma, immunologic diseases of the lung, transplantation associated diseases and infectious diseases such as RIV and hepatitis.
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                                                                                                                                                                                                                                                                                                                                                                                Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 0;
1; Mismatches
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              TTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGGATATAAAATTTTGTTGCC
                                                                                                                                                   rittaaaaaactgaatt---dgaatagaattggtaagtt---gcaaagacttttgaaa
                                                                                                                                                                                                                                                                                                                                                                                     cardiac hypertrophy; cardiovascular disorder; endothelial cell growth; angiogenic disorder; atherosclarensia; osteoporosas; hypertension; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cance Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal; ss.
                                                                   CTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA
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ark MR, Marsters SA;
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or
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genetic disorders and treating cardiovascular, endothelial or
angiogenic disorders, such as atherosclerosis, wounds or cancer -
                                                                                                                                                                                                                                                                                                                                                             Human angiogenesis-associated protein PRO200 cDNA, SEQ ID NO:50.
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AL, Hillan KJ, Kuo SS, Mark MR, M
Watanabe CK, Williams PM, Wood WI;
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99US-0123957.
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Pitti RM,
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P-PSDB; AAB53074.
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02-JUN-1999;
23-JUN-1999;
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26-JUL-1999;
01-SEP-1999;
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15-SEP-1999;
05-OCT-1999;
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30-NOV-1999;
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12-MAR-1999,
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Claim 58; Fig 21A-B; 293pp; English.

The invention letates to mover numen auglosquestreas processing designated PRO proteins (AABS)064-851097), and to nucleic acids encoding PRO proteins (AABS)064-851097), and to nucleic acids encoding PRO proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, from antibodies specific for a PRO protein, fusion proteins compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO expression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a particular tissue; treating a cardiovascular, endothelial or angiogenic disorder or an endothelial or angiogenic disorder or an endothelial or angiogenic or an endothelial or angiogenist or antagonist a retroviral gene therapy vector comprising compounts or and methods of inhibiting or stimulating endothelial or PRO agonist or and methods of inhibiting or stimulating endothelial or administration of a PRO protein, and methods of inhibiting or stimulating endothelial or administration of a PRO protein, and methods of inhibiting or stimulating endothelial or administration of a PRO protein, and administration of a PRO proteins, and administration of a PRO proteins, and admerioals, ulcers, wounds, cancer, Alzheimer's disease, Huntington's endometrioais, ulcers, wounds, cancer, Alzheimer's disease, produced angiogenic disease, or stroke. PRO proteins, are additionally useful in the recombinant production of PRO proteins, as and appeare encoding PRO proteins, to analyse genet to produce transgenic company. PRO nucleic acids and also be used to produce transgenic c invention relates to novel human angiogenesis-associated proteins protein of the invention.

Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;

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Best Local Similarity 97.7%;
Matches 2059; Conservative 250 62 122 302 422 182

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790	AAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 849
602	CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCGAGAGATGGC 661
662	AGTIGGACTIAGAAGAICTATATAGGCCAACTIGGCAACTICTTGGCAAGGCTTTTGTTT 721
722	TIGGAAGAAATCCAGAGIGGIGGAICIGAACCTICTAACAGAGGGAAGGIAAGATTAIACA 781
782	GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841
842	TITICIGACCAGGITGICICCIGGITAAACGCIGIGGGAACIGIGCCIGITGICCC 901
902	ACAATTGCAATGAATGTCAATGTGTCCCAAGGAAAGTTACTAAAAAATACCACGAGGTCC 961
962	TTCAGTTGAGACCAAAGACCGGGGGTCAGGGGATTGCACAAATCACTCAC
1022	TOGAGCACCATGAGGAGTGTGACTGTGTGTGTGAGGAGCACAGGAGGATGAGGATC 1081
1082	ACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCGTGGCTGATTCTATTAGAGAACGT 1141
1142	ADGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTGATCTTCAGGAT 1201
1202	TTACAGTGCATTCTGAAAGAGGAGACTTCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1261
1262	TTGAGAGGAGGCCTAAAGGACAGGAGAAAGGTCTTCAATCGTGGAAAGAAA
1322	TIGIATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
1382	GITCIGIAITITCAGITCITICGAIACGCITAGGGIAAIGICAGIACAGGAAAAAACIG 1441
1442	TGCAAGTGAGCACTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1501
1502	
1562	AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621

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2000WO-US04414.
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2000WO-US05004.
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2000WO-US06319.
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                                    98WO-US24855.
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99WO-US05028.
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99WO-US28565.
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25-MAY-2001; 2001WO-US17092.
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22-JUN-2001; 2001WO-US20116.
29-JUN-2001; 2001WO-US21066.
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20-DEC-2000; 2000US-0747259.
28-FEB-2001; 2001US-0796498.
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14-MAR-2001; 2001US-0808689.
22-MAR-2001; 2001US-0816744.
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10-MAR-1999;
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14-MAY-1999;
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1622 ACTIGIGICRIGCIGATAGGACAGACIGGATTITICATATITCITATIAAATITCTGC 1681
                                                    1870 ACTIGIGIGICALGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAATTTCTGCC 1929
                                                                                         1682 ATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAGAGTGG 1741
                                                                                                      1930 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1989
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cDNA encoding human PRO polypeptide #143.
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98WO-US12456.
98WO-US17882.
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98WO-US19177.
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The present invention relates to the isolation of novel human PRO polypeptides, and the polymucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides are useful for detecting other PRO polypeptides, for inking bloactive molecules to cells expressing PRO polypeptides, for for modulating biological activities of cells expressing PRO polypeptides, for identifying agonists or antagonists.

The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TNF)-alpha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polymuclectide sequences encoding PRO polypeptides are useful as hybridiaation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the generation analysis of individuals with genetic disorders, and in gene therapy, ACA0360-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic format directly from the property.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGAA 181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification -
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches
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              2001US-0854208.
2001US-0854280.
2001US-08660216.
2001US-0866034.
2001US-0872035.
2001US-0872035.
2001US-0872035.
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2001US-0924419.
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16-AUG-2001; 2001US-0931836.
19-DEC-2001; 2001US-0028072.
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Smith V, Stewart TA, Tum
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P-PSDB; ABU66712.
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18-JUL-2001; 2
06-AUG-2001; 2
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430 TIATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 489
                                     301
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                                                                                                                                                                                                                                                                                               670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 729
                                                                                                              CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG 361
                                                                                                                                                                                                                                                                                                                                                          790 AAGCIGIGAGICCTICAGIGCTACCCCCTICAGCTTIGCCACTGGACCTGATAATG
                                     GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA
                                                                                                                                 610 TAGAAGTTGAAGCACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG
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                                  Homo sapiens,
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                                                                                                                                                                      GIICTOTAITICAGIICTITCGAIACGGCTIAGGGTAAIGICAGTACAGGAAAAAACTG 1441
                                                                                                                                                                                                                                           1630 GITCIGIATITCAGITCITICGATACGGCTTAGGGTAATGICAGTACAGGAAAAAACTG 1689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           152 AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1621
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                              TIGIAITAAATAGAICACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 1381
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                                                                    1570 TIGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG
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                                                                                                                                                                                                                                                                                                               1442 IGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGGCCT
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2000WO-US22031
03-MAY-2002; 2002US-0137865
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Claim 2; Fig 285; 659pp; English.
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2001US-0802706.
2001US-080E89.
2001US-081E744.
2001US-0858366.
2001US-0854209.
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2001US-0872035.
2001US-0874503.
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2000US-0747259,
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ME, Goddard
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                                                                                                                                                                                                                                                          Stewart TA,
                                                                                                                                                                                                                                 (GETH ) GENENTECH INC.
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18-JUL-2001;
06-AUG-2001;
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      24-AUG-2000;
08-NOV-2000;
                  10-NOV-2000;
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Gerritsen
                                                                                                                                                                                                                                                          Smith V,
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Eaker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; WPI; 2003-313925/31.

P-PSDB; ABU66988.

When secreted and transmembrane nucleic acids and polypeptides, designated as FPO; useful for treating inflammation, organ failure, atherosolerosis, cardiac injury, infertility, birth defects, premature approacherosis, cardiac injury, infertility, birth defects, premature approacherosis, cardiac contact of the International Contact of Contact Secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited under American Type Culture Collection (ArCC) accession number in a list given in the specification. Also included are vectors and host contact of proteins, PRO proteins, PRO conting PRO proteins, PRO continged are vectors and host of the proliferation of deferentiation of chondrocyte cells, the rolleration of deferentiation of chondrocyte cells, the proliferation of differentiation of chondrocyte cells, the proliferation of deferentiation of chondrocyte cells, the proliferation of deferentiation of chondrocyte cells, the proliferation of deferentiation of chondrocyte cells, the proliferation of any period of monourclear cells, the release of a cyclokine from peripheral blood monourclear cells, the release of a cyclokine from peripheral blood monourclear cells, the release of a cyclokine from peripheral blood monourclear cells, the companied of the proliferation of adapted of monourclear cells, a method for mobile of adapted of a the differentiation of adapted of a method for mobile of adapted of a the differentiation of adapted of a cyclokine from peripheral pero

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1030 GCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAAGAACCGATACCA 1089 609 699 970 Triggaagaaatccagagrggrggrcrgaaccrrcraacagaggaggraagarraraca 1029 121 310 reacarcrecerredecedeceadacacadedecedecedaarccaaecreadera 369 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181 429 241 489 301 549 361 421 481 729 541 789 696 250 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCTGC 309 601 661 909 790 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 849 TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 781 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT 721 61 from any of the nucleotide sequences cited above. The nucleic acids and polypeptides are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or diabetic complications. The nucleic acids are useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. Both are useful in tissue typing.

The present sequence encodes a PRO protein of the invention. 2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCCAAATGAGCCTCTTCGGGCTTCTCCTGG 62 TGACATCTGCCCTGGCCGGCCAGAGACGAGGACTCAGGCGGAATCCAACCTGAGTAGTA TTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATCCAA GAAATACGGTCTTGGTATGGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 550 CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG 730 ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 610 TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG **TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT** 670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT ATTITICCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG 910 AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT 36; Indels 11; Gaps Query Match 93.9%; Score 1979.4; DB 25; Length 2849; Best Local Similarity 97.7%; Pred. No. 0; Matches 2059; Conservative 1; Mismatches 36; Indels 11; C Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other; 370 122 182 430 242 490 302 362 422 482 542 602 850 662 722 88888888888888ठे ద ઠે qq ð 셤 ઠે 엄 à ద õ 임 ò d ò g ò 셤 ò ď δ 셤 ò ద ઠે 셤 ò 셤

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'GGDZ_6/ptodata/2/ina/5A_COMB.seq:*
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'CGDZ_6/ptodata/2/ina/6A_COMB.seq:*
'CGDZ_6/ptodata/2/ina/BE_COMB.seq:*
'CGDZ_6/ptodata/2/ina/PCTUS COMB.seq:*
'CGDZ_6/ptodata/2/ina/PCTUS COMB.seq:*
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Sequence 151, App
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Sequence 287, App
Sequence 1, Appli
Sequence 3, Appli
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APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: BUDCHELLAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
FILE REFERENCE: P1122
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT FILING DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  224 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTCC 283
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           284 TGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCCAGGCGGAATCCAACCTGAGTAGTA 343
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US-08-988-197-8
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches
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OTHER INFORMATION: N is A, T, C or G
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; Patent No. 6391311
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1379 TTGAGAGGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGGAAATTAAATG 1438
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                                                                                                                                                                                                                                                                                                                                                                                                                                     842 TITICIGGCCAGGITGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCC 901
                                                                                                                                                                                                                                                                                 779 AGTIGGACTIAGAAGAICIATAIAGGCCAACIIGGCAACIICTIGGCAAGGCITIIGIII 838
                                                                                                                                                                                                                                                                                                                                                                                                             GCTGCACACCTCGTAACTTCTCAGGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACCA 841
                                                                AAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG 601
                                                                                                                                                   CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 661
                                                                                                                                                                                                                                                                                                                           TIGGAAGAAAAICCAGAGIGGIGGAICIGAACCITCIAACAGAGGAGGIAAGAITAIACA 781
                    ATTITICITICIAGAACCAGGGTTCTGCATCCACATTGTCATGCCACAATTCACAG 658
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1259 ATGCGTTATCTCCATCCTTAATCTCAGTTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TIGIATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG
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1262
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Patent No. 6495668
GENERAL INCORMATION:
APPLICANT: Glibert, Teresa
APPLICANT: Glibert, Teresa
APPLICANT: Bart, Charles E.
APPLICANT: BREPARAL PAIL O.
APPLICANT: BREPARAL PAIL O.
APPLICANT: BROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-01-10
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77.1%; Score 1624.8; DB 4; Length 1760;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1637; Conservative 1; Mismatches 3; Indels 1;
                                                                                                                                                                                                                                                               APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 90-60C1
CURRENT FILING DATE: 2000-11-06
PRIOR PILING DATE: 2000-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO!
LENGTH: 1760
                                                  1621 AACTTGTGTCRTGCTGATAGGA 1642
                                                                           Sequence 1, Application US/09706968 Patent No. 6528050
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ) NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-09-706-968-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                 GENERAL INFORMATION:
                                                                                                                                                                                 US-09-706-968-1
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1679 AAACCAGAAACATETATGTACTACAAACCTGGTTTTTTAAAAGGAACTATGTTGCTGTGT 1738
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                                                                                                                                                                                                                                                                                         839 TIGGAAGAAATICCAGAGIGGIGGATCTGAACCTICTAACAGAGGAGGAAGATAATAAA 898
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                                       659 AAGCIGIGAGICCTICAGIGCTACCCCTTCAGCTITGCCACIGGACCIGCTTAAIAAIG 718
                                                                                                                                 719 CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC 778
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               542 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCCACTGGACCTGCTTAATAATG 601
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                                                                                                                                                                    Geguence 1, Application US/09457066
Facent Co. 6432673
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Gao, Zeren
APPLICANT: Biddington, Christopher S.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: BLIBSTORMERS B.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REPERENCE: 98-06.
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Factor Windows Version 3.0
                                         1621 AACTIGIGICRIGCIGAIAGGA 1642
                                                               Matches 1637; Conservative
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LOCATION: (154)...(1191)
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US-09-457-066-1
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US-09-457-066-1
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                                                                                       680 ATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTTGGAAGAAAATCCA 739
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620 GTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGCAGTTGGACTTAGAAG 679
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APPLICANT: Gao. Zeren
APPLICANT: Gao. Zeren
APPLICANT: Bart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gaet, James W.
TILLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF3
FILLE REFERENCE: 98-6021
CURRENT APPLICATION NUMBER: US/09/706,968
FRICK APPLICATION NUMBER: US/09/541,752
FRICK APPLICATION NUMBER: US/09/541,752
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 50
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                                                                                                                                                                                                                                                                             APPLICANT: Gao, Zeren
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Briddington, Christopher S.
APPLICANT: Priddington, Christopher S.
APPLICANT: APPLICANT: Aboemaker, Kimberly E.
APPLICANT: Gibertson, Debra G.
APPLICANT: Gibertson, Debra G.
APPLICANT: Gibertson, Debra G.
TITLE OF INVENTION GROWTH FACTOR HOMOLOG ZVEGF3
CURRENT APPLICATION NUMBER: US/09/457,066
CURRENT FILIAG DATE: 199-112-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FASTSEQ for Windows Version 3.0
                                          1739 ATTAAACTTGTGTCGTGCTGATAGGA 1764
         1617 ATTAAACTTGTGTCRTGCTGATAGGA 1642
                                                                                                                                                                                                 Sequence 50, Application US/09457066 Patent No. 6432673 GENERAL INFORMATION:
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200 CTAAIGGAAGTAITCACAGCCCAAGGITTCCICATACTTAICCAAGAAAIACGGICTIGG 259
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                                                                      317 TTGGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTTGTAGAAGTTGAGGAAC 376
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RESULT 8
US-09-564-595D-34
IS-09-564-595D-34
Patent No. 649568
GENERAL INFORMATION:
APPLICANT: Glibert, Charles E.
APPLICANT: Sheppard, Paul O.
TILLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
FRIOR APPLICATION NUMBER: US/09/564,595D
FRIOR APPLICATION NUMBER: US/09/564,216
FRIOR FILING DATE: 1999-05-03
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45.5%; Score 959.4; DB 4;
Best Local Similarity 70.3%; Pred. No. 6.4e-235;
Matches 1446; Conservative 1; Mismatches 578;
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FILING DATE: 1999-11-10
PRIOR PILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 34
                                                                                                                                                                                                                                                                                                                                                                                                                                           ) NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-564-595D-34
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; LOCATION: (1049)...(2086)
US-09-706-968-42
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Best Local Similarity 70.3%; Pred. No. 6.4e-235;
Matches 1446; Conservative 1; Mismatches 578; Indels 31; Gaps
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| Sequence 42, Application US/09706968
| Patent No. 6528050
| General Information:
| APPLICANT: Hart, Charles E. APPLICANT: Piddington, Christopher S. APPLICANT: Sheepard, Paul O. S. APPLICANT: West, James W. TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF3 FILE REFERENCE: 98-60C1
| CURRENT APPLICATION WUMBER: US/09/706,968 | CURRENT APPLICATION NUMBER: US/09/541,752 | PRIOR APPLICATION NUMBER: US/09/541,752 | PRIOR PILING DATE: 2000-03-31 | NUMBER OF SEQ ID NOS: 50 | SOFTWARE: PastSEQ for Windows Version 3.0 | SEGIPMARE: PastSEQ for Windows Version 3.0 | LEMOTH.
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APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60.
CURRENT APPLICATION NUMBER: US/09/457,066
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SOFTWARE: FastSEQ for Windows Version 3.0
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Patent No. 6432673
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; LOCATION: (1049)...(2086)
US-09-457-066-42
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OTHER INFORMATION: 2

NAME/KEY: misc feature
LOCATION: (1) ... (1035)

OTHER INFORMATION: n = A,T,C or G
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US-09-706-968-6
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34.8%; Score 734.4; DB 4; Length 1035;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188; Indels 0;
                                                         APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOWOLOG ZVEGF3
FILE REFERENCE: 98-60
CURRENT APPLICATION WUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
WUMBER OF SEG ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
              APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
                                                                                                                                                                                                                                                                                                                                                   , LOCATION: (1) ... (1035); OTHER INFORMATION: n = A,T,C or G US-09-457-066-6
                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
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APPLICANT: Gao, Zeren
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697 CAACTICTIGGCAAGGCTTTTTGGAAGAAAAATCCAGAGIGGIGGAICTGAACCIT 756
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APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT FILING DATE: 2000-11-06
CURRENT FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
34.8%; Score 734.4; DB 4;
Best Local Similarity 56.6%; Pred. No. 8.9e-178;
Matches 585; Conservative 261; Mismatches 188;
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901 GTNACNAARAARTAYCAYGARGTNYTNCARYTNMGNCCNAARACNGGNGTNMGNGGNYTN 960
                                                            AACATTGTCATGCCACAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCT 576
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            277 GAGGAAAATGTATGGATACAACTTACGTTTGAAGATTTGGGCTTGAAGACCCCAGAA 336
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157 GTACAAGATCCTCAGCATGAGAGAATTATTACTGTGTCTACTAATGGAAGTATTCACAGC 216
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; Sequence 6, Application US/09564595D
; Patent No. 6495668
                                                                                    GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
RESULT 13
US-09-564-595D-6
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118 AGTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAG 177
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Best Local Similarity 34.5%; Pred. No. 8.2e-36;
Matches 349; Conservative 194; Mismatches 395; Indels 75; Gaps
APPLICANT: Sheppard, Paul O.
7 ITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REPERRICE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR PELLOR DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR PLLING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR PLLING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FREESEQ FOR WINDOWS VERSION 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEATURE:
OTHER INFORMATION: degenerate sequence
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LOCATION: (1). .. (1110)
OTHER INFORMATION: n = A,T,C or G
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463 AGATTTGTATCTGATGAATATTTTCCTTCTGAACCAGGTTCTGCATCCACTACAACATT 522
                                                       523 GT----CAIGCCACAATICACAGAAGCIGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTT 578
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Patent No. 6495668
GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OP INVENTION: GROWTH FACTOR HOWOLOG ZVEGF4
FILE REFERENCE: 99-19
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CURRENT FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 1999-11-10
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR APPLICATION NUMBER: US 60/180,169
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FRASESEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                169 CAGCATGAGAGTATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCT 228
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                                                                                                                      781 AGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATACC 840
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5.6%; Score 117.8; DB 4; Length 1472;
Best Local Similarity 50.9%; Pred. No. 1.6e-20;
Matches 494; Conservative 0; Mismatches 402; Indels 75; Gaps
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APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4
FILE REFERENCE: 00-28
CURRENT APPLICATION NUMBER: US/09/540,224
CURRENT FILING DATE: 2000-03-31
BARLIER APPLICATION NUMBER: US 60/180,169
EARLIER PILING DATE: 2000-02-04
NUMBER OF SGO ID NOS: 9
SOFTWARE: FASTSEQ for Windows Version 3.0
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Patent No. 6468543
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ORGANISM: Mus musculus
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ORGANISM: Mus musculus

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   303 AACAGCTACCCAAGGAACCTGCTTCTGACATGGTGGCTCCGTTC---CCAGGAGAAAACA 359
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     289 TGGATACAACTTACGTTTGATGAAGATTTGGGCTTGAAGACCCGGAAGATGACATATGC 348
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                                                                                                                                                                                         Query Match
5.6%; Score 117.8; DB 4; Length 1472;
Best Local Similarity 50.9%; Pred. No. 1.6e-20;
Matches 494; Conservative 0; Mismatches 402; Indels 75; Gaps
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (93)...(1205)
US-09-564-595D-52
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Search completed: November 26, 2003, 05:52:12

Job time: 116.97 secs
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Perfect score:

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Scoring table:

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APPLICANT: AASI, KAIIN
APPLICANT: PONTEN, ANDICA
APPLICANT: PONTEN, ANDICA
APPLICANT: UUTELA, MATKO
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APPLICANT: UUTELA, MATKO
APPLICANT: OBSTWAN, ARD
APPLICANT: HELDIN, CAT!-HENTIK
APPLICANT: 1034-10349-ETIKSSON et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
FRIOR APPLICATION NUMBER: 00/110,749
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR APPLICATION NUMBER: 50/100/1002
PRIOR PRIO
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LOCATION: (2002)
OTHER INFORMATION: can be a, c, g
     APPLICANT: ERIKSSON, U1F
APPLICANT: AASE, Karin
APPLICANT: LEE, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: UUTELA, MARKO
APPLICANT: ALITALO, Kari
APPLICANT: OSSTWAN, Anne
 TYPE: DNA
ORGANISM: Homo sapiens
   -09-852-209A-2
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                                                                                                            2003, 03:42:52 ; Search time 518.968 Seconds (without alignments) 13382.717 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpna/USO7_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/CTN_EW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
4: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
5: /cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*
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Compugen Ltd.
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                           CACAATTGCAATGAATGTCAATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGGTC
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Qy 1981 CCTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGC 2040 	Qy 2041 ATTTTAAAAACCTGAATTGGGAANGGAANTTGGTAAGGTTGGCCAAANCTTTTTTGAA 2100	2101 ATAATTAA 2108 	SULT 2	S-10-131-600-2 Sequence 2, Applicati Publication No. US200 GENERAL INFORMATION:	APPLICAN: EXELSSON, 01 APPLICANT: LEE, Xuri APPLICANT: LEE, Xuri APPLICANT: Annica APPLICANT: Merror	APPLI APPLI APPLI		CURREI PRIOR PRIOR		PRIOR PRIOR	PRIOR NUMBER SOFTWA						Query Match 99.8%; Score 2103.6; DB 14; Length 2108; Best Local Similarity 100.0%; Pred. No. 0; Matches 2108; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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             Sequence 1, Application US/10178442
| Publication No. US20030113870A1
| GENERAL INFORMATION:
| APPLICANT: Ferrara, Napoleone
| APPLICANT: Kuo, Sophia S.
| TITLE OF INVENTION: POLYEPPTIDES HOMOLOGOUS TO FILE REFERENCE: 11659.112USD2
| CURRENT APPLICATION NUMBER: US/10/178,442
| CURRENT FILING DATE: 1999-03-10
| PRIOR APPLICATION NUMBER: US 09/265,686
| PRIOR APPLICATION NUMBER: US 09/265,686
| PRIOR PILING DATE: 1998-11-02
| PRIOR FILING DATE: 1998-03-17
| PRIOR FILING DATE: 1998-03-17
| NUMBER OF SEQ ID NOS: 8
| SOFTWARE: PATENTIN NOS: 8
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: misc feature
LOCATION: (2689)..(2689)
OTHER INFORMATION: Any nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 2825
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PRIOR APPLICATION NUMBER: 09/514,010 PRIOR PILLING DATE: 2000-02-25 PRIOR PLILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: 09/516,745 PRIOR PLILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: 09/572,002 PRIOR PLILING DATE: 2000-05-14 PRIOR PLILING DATE: 2000-05-19 PRIOR PLILING DATE: 2000-06-29 PRIOR PLILING DATE: 2000-06-29 PRIOR PLILING DATE: 2000-06-29 PRIOR APPLICATION NUMBER: 09/60,565 PRIOR PLILING DATE: 2000-07-31 PRIOR PLILING DATE: 2000-06-29 PRIOR PLILING DATE: 2000-06-29 PRIOR PLILING DATE: 2000-06-29 PRIOR PLILING DATE: 2000-06-29 PRIOR PLILING DATE: 2000-09-30 PRIOR PLILING DATE: 2000-09-30 PRIOR PLILING DATE: 2000-09-20 PRIOR PLILING DATE: 2000-09-30	S-047/96-75 Suery Matc Query Matc Best Local Best Local Best 10cal Atches 20 Y Y Y Y Y Y Y Y Y Y Y Y Y

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R APPLICATION NUMBER: 60/079728

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R APPLICATION NUMBER: 60/077641

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R APPLICATION NUMBER: 60/07791

R FILING DATE: 1998-03-13

R APPLICATION NUMBER: 60/07886

R FILING DATE: 1998-03-20

R APPLICATION NUMBER: 60/07886

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R FILING DATE: 1998-03-20
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APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080333
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081203
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     ATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGGTGG 1741
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                                               artragaagaagaactacarrcarggrrrggaagagaraaccrgaaaagagagrgg
                                                                                                       CCTTATICTTICACTTTATICGATAAGTICAGTTTATITTGTTTICATTGTGTACATTTTTATATT
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CURRENT APPLICATION NUMBER: US/09/978,295A
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PRIOR APPLICATION NUMBER: 09/918585
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Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
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Ferrara, Napoleon
Filvaroff, Ellen
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Gao, Wei-Qiang
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Desnoyers, Luc
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APPLICANT: Baker Kevin P.
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TIGGAAGAAATCCAGAGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA 1029 429 489 549 609 699 789 309 241 541 121 369 181 301 361 481 729 849 661 909 721 696 421 601 781 61 2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG TGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTA 550 CGTTTGATGAAAGATTTGGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTTG TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG 670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT ATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG 730 ATTITICCTICIGAACCAGGGTICIGCAICCACTACAACATIGICATGCCACAATICACAG 790 AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG TGACATCTGCCCTGGCCGGCCAGAGGACGAGGACTCCAGGCGGAATCCAACCTGAGTA 370 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 430 TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCCAAGGTTTCCTCATACTTATCCAA GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA CGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG TAGAAGTTGAGGAACCCAGTGAAGTATATTAGGGCGCTGGTGTGGTTCTGGTACTG TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT AAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATAATG CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGATGGC AGTIGGACITAGAAGAICTATATAGGCCAACTIGGCAACTICTIGGCAAGGCTITIGITT AGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTT TTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACA Gaps DB 10; Length 2849; 11; 36; Indels Score 1979.4; Pred. No. 0; 1; Mismatches PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FLING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR APPLICATION NUMBER: 60/085689
PRIOR FILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15 Query Match 93.9%; Best Local Similarity 97.7%; Matches 2059; Conservative 362 422 62 310 122 182 490 610 482 542 850 722 242 302 602 662 910 970 셤 à a ð g 8 6 g ò g ð g Š g 8 셤 à g ठे ద ð ద à õ

	RESULT 6 US-09-978-697-487 ; Sequence 487, Application US/09978697 ; Sequence 487, Application US/09978697 ; Patent No. US20020169284A1 ; GENRRAL INFORMATION: ; APPLICANT: Baker Kevin P. ; APPLICANT: Bestein, David ; APPLICANT: Bestein, David ; APPLICANT: Bestein, David ; APPLICANT: Exten, Dan ; APPLICANT: Frivareff, Ellen ; APPLICANT: Fong, Sherman ; APPLICANT: Fong, Sherman ; APPLICANT: Gackow, Mary E. ; APPLICANT: Gackow, Panageter ; APPLICANT: Gackow, Ranada, J. Christopher ; APPLICANT: Glurney, Austin L. ; APPLICANT: Glurney, Austin L. ; APPLICANT: Kliavin, Ivar J.	No. Sopinity and the factor of	; PRIOR APPLICATION NUMBER: 60/077632 ; PRIOR FILING DATE: 1998-03-11 ; PRIOR APPLICATION NUMBER: 60/077641 ; PRIOR FILING DATE: 1998-03-11
	1082 ACCACCAGCAGCTCTTGCCCAGAGCTGCAGTGCAGTGCTGATTCTATTAGAGAACGT 1141 1330 ACCACCAGCAGCTCTTGCCCAGAGCTGCAGTGCCTGATTCTATTAGAGAACGT 1141 1342 ATGGGTTATCTCCATCCTTAATCTCTGCAGTGCCTGATTCTTTCATTCA	1630 GTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCGTACAGGAAAAAACTG 1689 1442 TGCAAGTGACCACCTGATTCCGTTGCCTTACCTTAACTCTAAGCTCCTGGGCCT 1501 1690 TGCAAGTGAGCACCTGATTCTTTTTTTTTTTTTTTTTTT	2050 CTCCTTTTGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATCTTTTTTTT

PRIOR APPLICATION NUMBER: 60/077491
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R APPLICATION NUMBER: 60/084366
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R APPLICATION NUMBER: 100/08444 R FILING DATE: 1998-04-22 R APPLICATION NUMBER: 60/082700 R FILING DATE: 1998-04-22 R FILING DATE: 1998-04-22 R FILING DATE: 1998-04-22 R APPLICATION NUMBER: 60/082796 APPLICATION NUMBER: 60/084639 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/085339 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085338 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085323 APPLICATION NUMBER: 60/085580 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085573 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/084600 FILING DATE: 1998-5-07 APPLICATION NUMBER: 60/084627 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085700 FILING DATE: 1998-05-15 FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083554
FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083558 FILING DATE: 1998-05-06 APPLICATION NUMBER: 60/084637 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/085582 FILING DATE: 1998-04-23 APPLICATION NUMBER: 60/083336 FILING DATE: 1998-04-27 APPLICATION NUMBER: 60/084598 60/084643 APPLICATION NUMBER: 60/085689 APPLICATION NUMBER: 60/085579 APPLICATION NUMBER: 60/082704 FILING DATE: 1998-04-22 APPLICATION NUMBER: 60/083322 FILING DATE: 1998-04-28 APPLICATION NUMBER: 60/082804 'ILING DATE: 1998-05-15 FILING DATE: 1998-05-15 FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/ FILING DATE: 1998-05-07 FILING DATE: 1998-05-07 FILING DATE: 1998-04-21 PRIOR PRIOR

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93.9%; Score 1979.4;
Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches
 PRIOR APPLICATION NUMBER: 60/085704
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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R FILING DATE: 1998-03-20
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R FILING DATE: 1998-03-25
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APPLICATION NUMBER: 60/079689
FILING DATE: 1998-03-27
APPLICATION NUMBER: 60/079663
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APPLICATION NUMBER: 60/082796
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APPLICATION NUMBER: 60/083336
FILING DATE: 1998-04-27
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APPLICATION NUMBER: 60/080334
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APPLICATION NUMBER: 60/081955
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APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/081049
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APPLICATION NUMBER: 60/081195
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APPLICATION NUMBER: 60/081203
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081819
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APPLICATION NUMBER: 60/080327
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APPLICATION NUMBER: 60/081071
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APPLICATION NUMBER: 60/082804
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APPLICATION NUMBER: 60/082700
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TITLE OF INVENTION: Scretced and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REPERENCE: PS-2030PLC9

FILE REPERENCE: PS-2030PLC9

CURRENT APPLICATION NUMBER: US/09/978,192A

CURRENT FILING DATE: 2001-10-15

PRIOR APPLICATION NUMBER: 00/06220

PRIOR APPLICATION NUMBER: 60/06220

PRIOR APPLICATION NUMBER: 60/06314

PRIOR FILING DATE: 1997-11-03

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/06364

PRIOR FILING DATE: 1997-11-21

PRIOR APPLICATION NUMBER: 60/07740

PRIOR PILING DATE: 1998-03-10

PRIOR PILING DATE: 1998-03-11

PRIOR PILING DATE: 1998-03-12

PRIOR PILING DATE: 1998-03-13

PRIOR PILING DATE: 1998-03-13
    2285 TTTTAAAAAACTGAATT---GGAATAGAATTGGTAAGTT---GCAAAGACTTTTTGAAAA 2338
                                                                                                                                                                                Sequence 487, Application US/09978192A
Patent No. US20020177553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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PRIOR APPLICATION NUMBER: 60/078910
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Ferrara, Napoleon
Filvaroff, Ellen
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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Gao, Wei-Qiang
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122 ANTICCAGGACCAGGACAGAGACAGGAGACTCAGGAGAACCAGGAGAA 129 130 AATICCAGGATCACCAGGAGACAGAGACAGAGACACCAGGAGAA 129 130 AATICCAGTTTTCCAGCAACAGAGACAGAACCAGAGACTCCAGCACCACCAGGAGAA 129 131 TANTACTGTGTCACTACTAATGGAAGTTATCAGGCCCAAGGTTTCCTCATACTATCCAA 149 132 GAAATACCAGTTTTGCACACAAGAAGATACCAGCCCAAGGTTTCCTCATACTTATCCAA 149 133 CGTTTGATCAGATTTGAGAAGTTATCACAGCCCAAGGTTTCCTCATACTTATCCAA 149 134 GAAATACGGTCTTGATAGAAGTTATCACAGCCCAAGGTTTCCTCATACTTATCCAA 149 135 CGTTTGATCAGACTTTGATAGAAGTTATCAGACTAAGAGTTACCAAGTTTCCTCATACTTTATCCAA 149 136 CGTTTGATCAGACATTTGATAGAAGTTATCAGACTAAGAATTTCCTCATACTTTATCAA 149 137 CGTTTGATCAGACATTTGATAGAACTTAAGAAGTTACCAAGTTATCCTCATACTTTATCAA 149 138 CGTTTGATCAGAACTTTGATAGAACTTAATAAGACCCCCAAAGATAACCAAGTTACCAAGTTATCTAACTTATCAACTTTA 149 139 CGTTTGATCAGAACTTTGATAGAACTTAATAAGACCCCCAAGATAACTTACCAAGTTATCTAACTTATCAACTTA 149 140 CATTTGATCAGAACACTTAAACAAATTATAAGACCCCTTGAACTTTTCCTCAATACTTTTCTAACTTATCAACTTA 149 140 CATTTGATCAGAACACTTCAAACAAAATTAAAAATTACCAAGTTATCTAACTTATCAACTTA 149 141 CATTTGATCAGAACACTTCAAACAAAATTACAACATATCCAAATTACCAAATTACCAAATTACCAAATTACAACTTAAACTACAAATTACAACTTAAACAAAAAA	TCGAGCACCATGAGGGGTGTCAGGGGATTGCACAAATCACTCAC
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APPLICATION NUMBER: FILING DATE: 1998-0 APPLICATION NUMBER:	ΣΟω

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Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
                                                                  Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Gerritsen, Mary E.
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Kuo, Sophia S.
Napier, Mary A.
Baker Kevin P.
Botstein, David
Desnoyers, Luc
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                                                      Eaton,
                  APPLICANT:
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 1390 ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1449
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                                    TTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT
                                                                    TTACAGTGCATTCTGAAAGAGGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT
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TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic IITLE OF INVENTION: Acids Encoding the Same CURRENT APPLICATION NUMBER: US/09/999,832A CURRENT FILING DATE: 2001-10-24 PRIOR PAPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-03
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PRIOR PELING DATE: 1998-03-25
PRIOR PELING DATE: 1998-03-26
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27 Tumas, Daniel Williams, P. Mickey Wood, William I.

Sequence 487, Application US/0999932A Publication No. US20020192706A1 GENERAL INFORMATION: APPLICANT: Ashkenazi, Avi

US-09-999-832A-487

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PRIOR APPLICATION NUMBER: 60/07920
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-20
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR PILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080154
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-05
PRIOR PILING DATE:
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250 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCCAATGAGCCTCTTCGGGCTTCTCCTGC 309 THATTACTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA 489 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAAAAAATGTATGGATACAACTTA 301 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 62 TGACATCTGCCCTGGCCGGCCAGAGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA Gaps Length 2849; 11; 36; Indels DB 10; 93.9%; Score 1979.4; 97.7%; Pred. No. 0; iive 1; Mismatches PRIOR PILING DATE: 1998-04-29
PRIOR APPLICATION NUMBER: 60/08359
PRIOR APLICATION NUMBER: 60/08359
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PRIOR APLICATION NUMBER: 60/08350
PRIOR PILING DATE: 1998-04-29
PRIOR PILING DATE: 1998-04-30
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PRIOR PLING DATE: 1998-05-05
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R FILING DATE: 1998-04-22

R APPLICATION NUMBER: 60/082797

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R APPLICATION NUMBER: 60/082796

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R FILING DATE: 1998-04-28

R FILING DATE: 1998-04-28

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R PILING DATE: 1998-04-08
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R FILING DATE: 1998-04-21
R APPLICATION NUMBER: 60/082569
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R APPLICATION NUMBER: 60/082704
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R PILING DATE: 1998-04-29
R APPLICATION NUMBER: 60/083559
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R FILING DATE: 1998-04-29
                          APPLICATION NUMBER: 60/080327
FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/084414
FILING DATE: 1998-05-06
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FILING DATE: 1998-04-01
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APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
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APPLICATION NUMBER: 60/081952
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APPLICATION NUMBER: 60/081838
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FILING DATE: 1998-04-22
APPLICATION NUMBER: 60/082700
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     FILING DATE: 1998-03-31
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APPLICATION NUMBER: 60/080165
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                                                                                                                                                                                              Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                   Paoni, Nicholas F
                                                                                                                    Napier, Mary A.
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APPLICATION NUMBER: 60/08441 APPLICATION NUMBER: 60/08441 FLILING DATE: 1998-05-06 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084640 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/084600 APPLICATION NUMBER: 60/084607 APPLICATION NUMBER: 60/08463 FILING DATE: 1998-05-07 APPLICATION NUMBER: 60/08463 APPLICATION NUMBER: 60/08463 APPLICATION NUMBER: 60/08538 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/08538 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/08532 FILING DATE: 1998-05-13 APPLICATION NUMBER: 60/08558 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/08559	b. 93.9%; Score 1979.4; DB 11; Length 2849; Similarity 97.7%; Pred. No. 0; Sy Conservative 1; Mismatches 36; Indels 11; Gaps CCCGCGGGGGGGGGCCCGGGCGAATGACCTCTCGGGCTTCTCCGG CCCGCCGTGAGTGACTCTCACCCCAGTCAGCCCAATGACCTCTTCGGGCTTCTCCTGC CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCCAATGACCTCTTCGGGCTTCTCCTGC CCCGCCGTGAGTGAGCTCTCACCCCAGGCGAATCCACCTGAGTAGTA 1 TGACATCTGCCTGGCCGGCCAGAGACGAGCGCTCAGGCGGAATCCAACCTGAGTAGTA 1 TGACATCTGCCTGGCCGGCCAGAGACGAGCGCCCAAGGCGCAATCCAACCTGAGTAGTA 1 TGACATCTGCCTGGCCGGCCAGAGACAGAACGGACTCAGGCGGAATCCAACCTGAGTAGTA 1 AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGGAACACTGAGTAGTA 3 AATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGGAACCCCAAGGTACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAGGAACAAAGGAAACAAGGAAAGGAAAATCAAGAAATAACAGTTTCCACTAACTA
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CURRENT APPLICATION WUBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
Prior Application removed - See File Wrapper or Palm
SEQ 1D NO 487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA
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Pred. No. 0;
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Best Local Similarity 97.7%; Pred. No. 0;
Matches 2059; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: unknown base US-09-978-608A-487
                                                                                                                                                                                            ORGANISM: Homo sapiens
                                                                                                                                                                                                                                    NAME/KEY: unsure
LOCATION: 2715
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                                                                                                      ACTIGIGECATGCTGATAGGACAGACTGGATTTTTCATATTTCTTATTAAAATTTCTGCC
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          AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA
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Publication No. US20030045462A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Farzara, Mapoleon
APPLICANT: Frizara, Mapoleon
APPLICANT: Fong, Sherman
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Filvaroff, Ellen
Fong, Sherman
Gac, Wei-Clang
Gerritsen, Hanspeter
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
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Roy, Margaret Ann
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Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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US-09-978-608A-487
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CURRENT APPLICATION NUMBER: US/09/978,585A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
Prior Application removed - See File Wrapper or Palm
SEQ ID NO 487
LENGTH: 2849
2110 AAAGGIATTTAATATTTTTTATGACAACTTAGATCAACTATTTTTAGCTTGGTAAAT
                                                                            2170 TTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATG---ATATAAAATATTGTTGC
                                                                                                                                  1982 CTCGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAACCTGCA
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                                                                                                                                                                                                         2042 TITIAAAAACCIGAATIGGGAANGGAANTIGGIAAGGIIGGCCAAANCTITITIGAAAA
                                                        TITICIAAACACAATIGITATAGCCAGAGGAACAAAGAIGGATAIAAAAATATIGITGCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       93.9%; Score 1979.4;
97.7%; Pred. No. 0;
live 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Forg, Sherman
Gao, Wei-Ciang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kujavin, Ivar J.
Kujavin, Ivar J.
Kujavin, Ivar J.
                                                                                                                                                                                                                                                                                                                                                                                                                  ; Sequence 487, Application US/09978585A; Publication No. US20030049633A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 2715
OTHER INFORMATION: unknown base
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Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botterin, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan
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Matches 2059; Conservative
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ORGANISM: Homo sapiens
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US-09-978-585A-487
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APPLICANT:
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       841
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                                                                                                                                                        902 ACAATTGCAATGAATGTCTCTCCCAAGCAAAGTTACTAAAAATACCACGAGGTCC
                                                                                                                                                                                                                                ATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT
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                         ACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCTGGTTGTTCTATTAGAGAACGT
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1330	1390 AIGCGITAICTCCAICCITAAICTCAGITGITTGCTTCAAGGACCTTTCATCTTCAGGAT 1 1202 TTACAGIGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCTCTT 1	1450 1262 1510	1322 TIGTATTAAATGACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG 	1382	1912 IGANGIGADE CONTROLLINGUIDE CONTROLLANDO		1810 AGAACATTCTATGTACTACAAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA	1672 ACTIGIGICKIGCIGAIAGGACAGATITICAIATTICAIATTAAAATTICTGCC 1870 ACTIGIGICAIGCIGAIAGGACAGACIGGATTITICAIATTICAIATTAAAAATTICTGCC	1882 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAGGAGGGGGG 1930 ATTTAGAAGAAGAAACTACATTCATGGTTTGGAAGAGATAACCTGGAAAGAAGAAGGAGTGG	1742 CCTTATCTTCACTTTATCCATAAGTCAGTTTATTTCATTCA	1802 CTCCTTTGACATTATAACTGGCCTTTTCTAATCTTGTTAATATATAT	1862 BARGGRATTRARARITCTTTTTRAGACAACTTRAGATCAACTATTTTAGCTTGGTAAT	1922 TTTTCTAAACACAATTGTTATAGCCAGAGGAACAAAGATGGATATAAAAATATTGTTGCC	1982 CIGGACAAAAAIACAIGIAINICCAICCCGGAAIGGIGCIGCAGAIGAACIGCA 2227 TCIGACAAAAAIACAIGIATTT-CATICTCGTAIGGIGCIAGAGITAGATT-AATCIGCA	2042 IIIIAAA 2285 TTTAAA	y 2102 TAATTAA 2108 b 2339 TAATTAA 2345	RESULT 12
	121 369 181		301	361 609	IG 421 Db	481 729	541 789	601 849	661 909	721 969	781 1029	841 1089	901 1149	961 1209	1021 1269	rc 1081	1141
2 CCCGCCGTGAGCTCTCCCCCGAGCGAAATGAGCCTCTTCGGGCTTCTCCTGG	62 TGACATCTGCCCTGGCCGGCCAGAGACGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA 310 TGACATCTGCCCTGGCCGGCCAGAGACAGGGGGACTCAGGCGGAATCCAACCTGAGTAGTA 312 AATTCCAGTTTTCCAGCAAACAGAACAGAGAGTAGTACAACTCAGCATGAGTAGAA	370 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAAAAAAA	2 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGGGAAAATGTATGGATA 	302 CGTTTGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG 	362 TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGGTGGTTCTGGTACTG [422 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 	482 ATTTTCCTTCTGAACCAGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG	542 AACTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTCAATAATG	602 CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC	662 AGTIGGACITAGAAGAICTATATAGGCCAACITGGGAACTICTIGGGAAGGCITITGTIT 	722 TIGGAAGAAATCCAGAGTGGATCTGAACCTICTAACAGAGGAGGTAAGATTATACA 	782 GCTGCACACCTCGFAACTTCTCAGTGCCATAAGGGAAGAACTAAAGAGAACCGATACCA 	842 TITICIGGCCAGGITGICICCIGGITAAACGCIGIGGGAACTGIGCCIGITGICCC	902 ACAATTGCAATGAATGTCAATGTCCCCAAGCAAAGTTACTAAAAAATACCACGAGGTCC 	962 TTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCAC	1022 TGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGAGGACACAGGAGGATAGCGGCATC	1082 ACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTG

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APPLICANT: Williams, Dailer, Mickey
APPLICANT: Williams, Dailer, Mickey
APPLICANT: Williams, Dailer
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE REPRENEUE: P263019: 12010-12.

TITLE REPRENEUE: P263019: 12010-12.

PRIOR PAPLICATION NUMBER: 09/91885
PRIOR PAPLICATION NUMBER: 09/91885
PRIOR PAPLICATION NUMBER: 09/010-32.

PRIOR PAPLICATION NUMBER: 00/07439
PRIOR PRIOR PRILING DATE: 1997-11-23.

PRIOR PRING DATE: 1997-11-23.

PRIOR PRING DATE: 1997-11-20.

PRIOR PRING DATE: 1997-11-20.

PRIOR PRING DATE: 1997-11-20.

PRIOR PAPLICATION NUMBER: 60/07459
PRIOR PAPLICATION NUMBER: 60/07764

PRIOR PAPLICATION NUMBER: 60/07764

PRIOR PAPLICATION NUMBER: 60/07764

PRIOR PAPLICATION NUMBER: 60/07769

PRIOR PAPLICATION NUMBER: 60/07769

PRIOR PAPLICATION NUMBER: 60/07789

PRIOR PAPLICATION NUMBER: 60/07789

PRIOR PAPLICATION NUMBER: 60/07836

PRIOR PAPLICATION NUMBER: 60/07864

PRIOR PAPLICATION NUMBER: 60/07864

PRIOR PAPLICATION NUMBER: 60/07964
Sequence 487, Application US/09978191A
Publication No. US20030050239A1
GENERAL INPORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Boestein, David
APPLICANT: Equin P.
APPLICANT: Equin P.
APPLICANT: Eaton, Dan
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Williams, P. Mickey
Wood, William I.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wel-Qiang
Gerrber, Hanspeter
Gerritsen, May E.
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Paoni, Nicholas F
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PRIOR FILING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07968
PRIOR PILLING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07978
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-27
PRIOR FILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/09923
PRIOR PLING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/08015
PRIOR PLING DATE: 1998-03-31
PRIOR PLING DATE: 1998-04-01
PRIOR PLING DATE: 1998-04-05
PRIOR PRIOR D
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	422 TACCAGGAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT 481 670 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAGATTTGTATCTGATGAAT 729 482 ATTTCCTTCTGAACCAGGGTTCTGCATCCACTACAAATTGTCATGCACAATTCACAG 541 730 ATTTCCTTCTGAACCAGGGTTCTGCATCCACTACAAATTGTCATGCCACAATTCACAG 789 542 AAGCTGTGAGCTCTGCATCCCCCTTCTGCATCACACTTGTCATGCCACAATTCACAG 789	190 AAGCTGTGAGTCCTTCAGTGCTTTGCCACTGGACCTTGGATAATAATAATAATAATAATAATAATAATAATAATA	TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGGGGGGTAAGATTATACA TTGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGGGGGGGG	842 TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGGAAACTGTGCCTGTTGTCTCC 901 1090 TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCC 1149 902 ACAATTGCAATGATGTCTCCCAGGAAGTTACTAAAAAAAA	1022 TGGAGCACCATGAGGAGTGTGACTGTGCAGAGGAGCACAGGAGGATAGCCGCATC 1081	1142 AIGCGITAICTCCAICCTTAATCTCAGTTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1201 1390 AIGCGITAICTCCAICCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAGGAT 1449 1202 TTACAGTGCATTCTGAAAGAGAGAACATCAAACAGAATTAGGAGTTGTGCAACACACTCTT 1261
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PRIOR APPLICATION NUMBER: 60/083499 PRIOR FILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/083545 PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-29 PRIOR FILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29 PRIOR APPLICATION NUMBER: 60/08350 PRIOR PILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29 PRIOR PILING DATE: 1998-04-29		FALOR AFFLICATION NUMBER: 00/084940 PRIOR AFFLICATION NUMBER: 60/084598 PRIOR FILING DATE: 1998-05-07 PRIOR FILING DATE: 1998-05-07	PRIOR APPLICATION NUMBER: 60/085339	FILING DATE: 1998-05 APPLICATION NUMBER:	Match Match 93.9%; Score 1979.4; DB 11; Length 2849; ocal Similarity 97.7%; Pred. No. 0; s 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 2 CCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCTGGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGCTTCTCGGGGCTTCTCGGGGCTTCTCGGGGCTTCTCGGGGCTTCTCGGGGCTTCTCGGGGGG	310 310 122 370 182

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APPLICANT: GOTHER MANIES, AMERIA LIST APPLICANT: GOTHER MANIES, AMERIA LIST APPLICANT: GOTHER MANIES, AMERIA LIST APPLICANT: AMERIA LIST APPLICANT: AMERIA LIST APPLICANT: WOO, SOPILE S.

APPLICANT: NO, SOPILE S.

APPLICANT: NO, SOPILE S.

APPLICANT: NO, SOPILE S.

APPLICANT: NO, MANIES S.

APPLICANT: NO, MANIES S.

APPLICANT: Pan, James; P.

APPLICANT: Pan, James; P.

APPLICANT: Pan, James; P.

APPLICANT: Pan, James; P.

APPLICANT: WILLIAM: JAMES: JAMES: JAMES; P.

APPLICANT: WILLIAM: JAMES: JAMES: JAMES; P.

BRIOR PILLIAM: DATE: JAMES: JAMES: JAMES; P.

BRIOR PILLIAM: DATE: JAMES: J
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
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                                                                                                                                                    1690 TGCAAGTGACCCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1502 AAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTTTGTCATATTCACATATGTAAACC 1561
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAATTAA 1869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1870 ACTIGIGICAIGCIGAIAGGACAGACIGGAITITITCAIAITITCITAITAAATITICIGCC 1929
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1682 ATTTAGAAGAGAAGACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGGTGG 1741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1930 ATTTAGAAGAAGAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTTATATT 1801
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CICCITITIGACATTATAACTGTTGGCTTTTCTAATCTTGTTAAATATATTTTTTACC 1861
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         GITCTGIATTICAGIICTTICGAIACGGCITAGGGIAATGICAGIACAGGAAAAAACTG 1441
                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGGCCT 1501
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                                                                                        TIGIATIAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGG
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Publication No. US20030050240A1
GENERAL INFORMATION:
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Botstein, David
APPLICANT: Betsein, David
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Forny Sherman
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2102 TAATTAA 2108
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TAATTAA 2345
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PRIOR APPLICATION NUMBER: 60/080107
PRIOR PILLING DATE: 1998-03-31
PRIOR PILLING DATE: 1998-04-01
PRIOR PILLING DATE: 1998-04-09
PRIOR PILLING DATE: 1998-04-05
PRIOR PILLING DATE: 1998-04-05
PRIOR PILLING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/08126
PRIOR PILLING DATE: 1998-04-15
PRIOR PILLING DATE: 1998-04-22
PRIOR PILLING DATE: 1998-04-22
PRIOR PILLING DATE: 1998-04-22
PRIOR PILLING DATE: 1998-04-22
PRIOR PILLING DATE: 1998-04-29
PRIOR PILLING DATE: 19
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310 TGACATCTGCCCTGGCCGGCCAGAGACAGGGGACTCAGGCGGAATCCAACCTGAGTAGTA 369 250 cccccccraactcacccccacrcaacccaaraaccccrcrrcacccrcrrccacc TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACTG 421 122 AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAGAA 181 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301 TGACATCTGCCCTGGCCGGCCAGAGACGAGGGACTCAGGCGGAATCCAACCTGAGTAGTA 430 TTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATCCAA CGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTTG TTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCAA GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA CGTTTGATGAAAGATTTGGGCTTTGAAGACCCAGAAGATGACATATGCAAGTATGATTTTG Gaps Length 2849; 11; CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTT 36; Indels DB 11; Score 1979.4; Pred. No. 0; 1; Mismatches PRIOR PILING DATE: 1998-04-30
PRIOR APPLICATION NUMBER: 60/08436
PRIOR PILING DATE: 1998-05-05
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-06
PRIOR PILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/084639
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/084639
PRIOR PILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/08533
PRIOR APPLICATION NUMBER: 60/08532
PRIOR APPLICATION NUMBER: 60/08558
PRIOR APPLICATION NUMBER: 60/08558
PRIOR APPLICATION NUMBER: 60/08558
PRIOR PILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/08558
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08559
PRIOR PILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15 93.9%; Best Local Similarity 97,7 Matches 2059; Conservative Query Match Tocal Similarity 370 62 182 242 490 302 550 362 셤 ò g ò 셤 ð g ò g ö g à

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TAGGAAGTTGAAGGAATCTATATTAGGGGTGATGATTGTATCTGGTACTG TACCAGGAAACCAGTGAATCAAATTAGGATAAATTTGTATCTGATCTGATGATT TACCAGGAAAACCAGTTTCTCAAAGGAATCAAATTAGGATAAGATTTGTATCTGATCTGATGATT TACCAGGAAAACCAGGGTTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAGAATTCACACACA	1082 ACCACCAGAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGC

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R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081071
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081195
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R APPLICATION NUMBER: 60/081203
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081838
FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/082568
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083559
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FILING DATE: 1998-05-07
APPLICATION NUMBER: 60/084640
FILING DATE: 1998-05-07
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APPLICATION NUMBER: 60/081229
FILING DATE: 1998-04-09
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FILING DATE: 1998-04-15
APPLICATION NUMBER: 60/081817
FILING DATE: 1998-04-15
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APPLICATION UNMERR: 60/082569
FILING DATE: 1998-04-21
APPLICATION NUMBER: 60/082704
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APPLICATION NUMBER: 60/082700
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APPLICATION NUMBER: 60/082796
FILING DATE: 1998-04-23
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APPLICATION NUMBER: 60/083336
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APPLICATION NUMBER: 60/083322
FILING DATE: 1998-04-28
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
APPLICATION NUMBER: 60/083499
FILING DATE: 1998-04-29
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FILING DATE: 1998-04-29
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FILING DATE: 1998-04-30
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                      REPRESENTATION OF THE PRESENTATION OF THE PRES
              APPLICANT: SHELICANT: Windows Dailed by Applicant with the Control of Millian F. Windows Applicant: Wood, William I. TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic Conservation Woods will be applicant to the Conservation of Secreted and Transmembrane Polypeptides and Nucleic Conservation Woods will be applicant to the Conservation of Secreted and Transmembrane Polypeptides and Nucleic Conservation Woods will be applicant to Wood will be applicant to Woods will be applicant to Wood
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FILING DATE: 1998-04-01
APPLICATION NUMBER: 60/080334
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FILING DATE: 1998-04-01
Shelton, David L.
Stewart, Timothy A.
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PRIOR APPLICATION NUMBER: 60/084598 PRIOR FILING DATE: 1998-05-07 PRIOR PELING DATE: 1998-05-07 PRIOR PELING DATE: 1998-05-07 PRIOR PELING DATE: 1998-05-07 PRIOR PELING DATE: 1998-05-07 PRIOR PLING DATE: 1998-05-13 PRIOR PLING DATE: 1998-05-13 PRIOR PLING DATE: 1998-05-13 PRIOR PLING DATE: 1998-05-13 PRIOR PLING DATE: 1998-05-15	Dest March 93.9%; Score 1979.4; DB 11; Length 2849; Batch 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5; Matches 2059; Conservative 1; Mismatches 36; Indels 11; Gaps 5; 2 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG 61 Db 250 CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGC 309 C2 TACATCTGCCTGGCCGGCCAGAGACAGGGGGAATCCAACCTCAGGTAGTA 121 Db 310 TGACATCTGCCTGGCCAGCACAGGACAGGGGGAATCCAACCTCAGGTAGTA 369 OY 122 AATTCCAGTTTTCCAGCAACAGGACAGGGGGAATCCAACACTCAAGTAGTA 369 OY ATTCCAGTTTTCCAGCAACAAGAACAGAACAGATCCAAGATCCTCAACATGAGAAA 429 Db 370 AATTCCAGTTTTCCAGCAACAAGAACAGACACAGGATACCAACAACATCAAGAAAA 489 OY ATTCCAGTTTTCCAGCAACAAGAACAAGAACAACACCCCAAAGATCCTCAACAACAACAACAACAACAACAACAACAACAACA	Db 670 TACCAGGAAACAGAITTCTAAAGGAAATCAAATTAGGATAGGA

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PRIOR APPLICATION NUMBER: 60/064249
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1682 ATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGTGG 1741
                             1930 ATTTAGAAGAAAGAGAACTACATTCATGGTTTTGGAAGAGTAAAACTGAAAAGAAGAGTGG
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                                                                                          1742 CCTTATCTTCACTTTATCGATAAGTCAGTTTATTTGTTTCATTGTGTACATTTTATATT
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Filvaroff, Ellen
Fong, Sheman
Gac, Wel-Qiang
Garber, Hanspeter
Gedren, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
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PRIOR APPLICATION NUMBER: 60/085582
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

    (bases 1 to 2826)

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Contact: MGC help desk
Email: cgapbs.r@mail.nih.gov
Finsle Produrement: ClONTECH
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                                                                                                                       Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 41 Row: g Column: 9
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186 This clone has the following problem: frame shifted.
                                                        A., and Myers,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CTGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GTAGAAGTTGAGGAACCCAGTGACGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 2826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             73;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTT
  http://www-shgc.stanford.edu
(Dickson, Mark) mcd@paxil.stanford.edu
M., Schmutz, J., Grimwood, J., Rodriquez,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 1894.2; DB 11
Pred. No. 5.6e-298;
1; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AATTCCAGTTTTCCAGCAACAAGGAACAGAAC-
                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
mol_type="mRNA"
/mol_type="mRNA"
/dow_tolone="TWAGE:4614150"
/tissue_type="Kidney"
/clone_lib="NIH MGC_75"
/lone_lib="NIH MGC_75"
/note="Vector: pDNR-LIB"
a 519 c 591 g 846
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 94.8%;
Matches 2057; Conservative
                              Contact:
Dickson, R. M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            601
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NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: http://www-shgc.stanford.edu
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
R. M.
                                                                                                                                                                                                                                                         94305
                                                                                                                                                                                                                                                                                                                                                                                                                                                       found
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               156
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       --GGAGTACAAGATCCTCAGCATGAGAGA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAA 480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         96
                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be four through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 110 Row: p Column: 4
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 9994186
This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ACGITIGAIGAAGAITIGGGCTIGAAGACCCAGAAGAIGACATATGCAAGIATGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cececercadaderereaceceadreaceaaaaaaaacererreaceareree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGACATCTGCCCTGGCCGGCCAGAGGACGAGGCGGCGGAATCCAACCTGAGTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 <u> GTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTACT</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACGITTGATGAAAGATTTGGGCCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 11; Length 2655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         75;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AATTCCAGTTTTCCAGCAACAAGGAACAGAAC-------
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone="IMAGE:6527736"
/tissue type="Uterus, leiomyosarcoma"
/clone lib="NIH MGC 71"
/lab_host="DH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1892.4; DB 1
Pred. No. 1.1e-297;
1; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMV-SPORT6"
479 c 551 g 803 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1. .2655
/organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89.8%;
94.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 94.8 Matches 2056; Conservative
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ORIGIN
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Klausner, R.D., Collins, F.S., Wagner, L., Shenmen, C.M., Schuler, G.D.,
Klausner, R.D., Collins, F.S., Wagner, L., Schemen, C.M., Schuler, G.D.,
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,
Hopkins, R.F., Jordan, H., Moore, T., Wang, J., Haich, F.,
Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,
Staplecon, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,
Schetz, T.E., Brownstein, M.J. Usdin, T.B., Toshiyuki, S.
Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,
McKernan, K.J., Mallahy, S.J., Bosak, S.A., McEwan, P.J.,
Morley, K.C., Hale, S., Carcia, A.M., Gay, L.J., Hulyk, S.W.,
Villalon, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,
Fahey, J., Helton, E., Ketteman, M., Madan, A., Roung, A.C., Shevchenko, Y.
Bouffard, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smailus, D.E.,
Generation and initial analysis of more than 15,000 full-length
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                   CCATTTAGAAGAAGAACTACATTCATGGTTTGGAAGAGATAAACCTGAAAAGAAGAGT 1988
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 2655)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2226 GCTCTGACAAAATACATGTATT-CATTCTCGTATGGTGCTAGAGTTAGATT-AATCTG
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                                                                                                                                                                                                                                                                      Kawai, J. Shinagawa, A., Shibata, K., Yoshino, M., Itoh, M., Ishii, Y., Atakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Atakawa, T., Itashi, K., Yosawah, H., Kondo, S., Yamanaka, I., Saito, T., Osiobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Isawa, M., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaido, I., Pesole, G., Kochiwa, H., Wagner, L., Washio, T., Sakai, K., Okido, T., Furuch, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bojunga, N., Carninci, P., de Bonaldo, M., Brownstein, M.J., Bult, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D. A., Kamiya, M., Lee, N. H., Lyons, P., Narchionni, L., Mashima, J., Mazzarelli, J., Mombaerts, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, N., Saski, H., Schonbach, C., Seya, T., Shibata, Y., Stcoch, K., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Wynshaw Boris, A., Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizaki, Y.
Functional annotation of a full-length mouse cDNA collection and surfaces a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Hiramoto, K., Hiracaka, T., Hirozane, T., Hayashida, K., Inotani, Y., Inchi, W., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Naka, M., Nishi, K., Nomura, K., Murata, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohno, M., Ohno, M., Saltoh, H., Sakai, C., Sakai, K., Sahito, R., Saltoh, H., Sakai, C., Sakai, K., Sakai, K., Sahatoh, H., Tagawa, R., Shibata, K., Shinagawa, A., Shiraki, T., Tagami, M., Tagawa, A., Takamashi, F., Takaku-Akahira, S., Muramatsu, M., and Hayashizaki, Y., Toya, T., Yasunishi, A.,
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Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 3244)
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Please visit our web site for further details.
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                                                                                         TITLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1256 AAACCACGAGTCCTTCGGTGTTGCCCCCTTCATCTTTGTCATTGGACCTGCTCAACAATG 1315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1196 ATTTTCCATCTGAACCCGGATTCTGCATCCACTACAGTATTATCATGCCACAAGTCACAG 1255
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
dev stage="adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    361
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  896 rigicalcharatorgeraanggaagcarccacacaccocaagrirocrcaracaraccaa 955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 GAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAACTTA 301
                                                                                                                                                                                                                                               /note="unnamed protein product; platelet-derived growth factor, C polypeptide (MGD|MGI:1859631, GB|NM_019971, evidence: BLASTN, 99%, match=2691)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          302 CGTTTGATGAAAGATTTGGGCTTGAAGACCCCAGAAGATGACATATGCAAGTATGATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cecececasacidadecercacideceasacidadadecercercercasecerceree
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     776 TGACATCTGCCCTGGCCGGCCAAAGAACGGGGACTCGGGCTGAGTCCAACCTGAGCAGCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             362 TAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGTTTTGGTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1136 TGCCAGGAAAGCAGACTTCTAAAGGAAATCATATCAGGATAAGATTTGTATCTGATGAGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       602 CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAAATGAGCCTCTTCGGGCTTCTCCTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACATCTGCCCTGGCCGGCCAGAGGACGAGCTCAGGCGGAATCCAACCTGAGTAGTA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          482 AITTICCTICTGAACCAGGGIICTGCAICCACIACAACAIIGICAIGCCACAAIICACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    542 AAGCIGIGAGICCTICAGIGCIACCCCTICAGCITIGCCACIGGACCIGCTIAAIAAIG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 3244;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30;
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70.0%; Pred. No. 2.5e-146;
iive 1; Mismatches 585; I
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11;

358

181 418 241

298 121

61

478

538

361 598 421 658 481 718 541 778 601 838 661 898 721 958 781

301

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ICKYDFVEVEEPSDGSVLGRWCGSGTVPGKOTSKGNHIRIREVSDEYFPSEPGFCIHY
SIIMPQVTETTSPSVLPPSSLSLDLLNNAVTAFSTLEELIRYLEPDRWQVDLDSLYKP
TWOLLGKAFLYGKKSKVVNLNLLKEEVKLYSCTPRNFSVSIRBELKRTDTIFWPGCLL
VKRCGGNCACCLHNCNBCQCVPRKYTKKYHEVLQLRFKTGVKGLHKSLTDVALEHHEE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   959 ATGGGAAAAAAAGCAAAGTGGTGAATCTGAATCTCCTCAAGGAAGAGGTAAAACTCTACA 1018
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCTGCACCCCCGGAACTTCTCAGTGTCCATACGGGAAGAGCTAAAGAGAGACAGATACCA 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAAACTGTGCCTGTTGTCTCC 901
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCGCCCCGCGAGTGAGCCCTCGCCCCAGTCAGCCAAATGCTCCTCCTCGGCCTCCTCCTCCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGACATCTGCCCTGGCCGGCCAGAGAGGAGGACTCAGGCGGAATCCAACCTGAGTAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAAATATGGTGCTGGTGTGGAGATTAGTTGCAGTAGATGAAATGTGCGGATCCAGCTGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CATTTGATGAGAGATTTGGGCTGGAAGATCCAGAAGACGATATATGCAAGTATGATTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTTTCCATCTGAACCCGGATTCTGCATCCACTACAGTATTATCATGCCACAAGTCACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAACCACGAGTCCTTCGGTGTTGCCCCTTCATCTTTGTCATTGGACCTGCTCAACAATG
                                                                                                                                                                                                                                                                                                                                                                                                                                       CCCGCCGTGAGTGAGCTCTCACCCCAGTCAGCCAATGAGCCTCTTCGGGCTTCTCCTGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATGAAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reccaseaaagcagacricraaaggaaarcararcaggaraagarrigrarcreargag
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTITICCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCACAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGATGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CTGTGACTGCCTTCAGTACCTTGGAAGAGCTGATTCGGTACCTAGAGGCCAGATCGATGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AGGIGGACTIGGACAGCCTCTACAAGCCAACAIGGCAGCTTTTGGGCAAGGCTTTCCTGT
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                                                                                                                                                                                                                                                                                                                                                                                  31;
                                                                                                                                                                                                                                                                                                                                 DB 11; Length 2765;
                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                       Pred. No. 3.4e-146;
1; Mismatches 578;
                                                                                                                                                                                                                                                                                                                                 Score 959.4;
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                                                                                                                                          2738. .2743
/note="putative"
2765
                                                                                                                                                                                                                          /note="putative"
                                                                                                                       CDCVCRGNAGG"
                                                                                                                                                                                                                                                                                                                              45.5%;
ilarity 70.3%;
Conservative
                                                                                                                                                                                                                                                      593 C
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 1446; Conserv
                                                                                                                                               polyA_signal
                                                                                                                                                                                              polyA_site
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RHERVVTISGNGSIHSPKFPHTYPRNWVLVWRLVAVDENVRIQLTFDERFGLEDPEDD
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/clone_lib="RIKEN full-length enriched mouse cDNA library"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, M., Hiramoto, K., Hiracka, T., Hirozane, T., Hirozane, T., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Kotch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamura, M., Nishi, K., Nomura, K., Mumazaki, R., Ohno, M., Ohazo, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sagabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takada, Y., Tanaka, T., Tanada, A., Tayaki, P., Yasunishi, A., Muramatsu, M., and Hayashizaki, Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Group Phase I & II Team.
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
Nature 420, 563-573 (2002)
6 (bases 1 to 2765)
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                                                                                                                                                                                                                                                                                                                                   Functional annotation of a full-length mouse cDNA collection
Nature 409 (6821), 685-690 (2001)
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             Pesole, G.,
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URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
                Matsuo, Y., Nikaido, I.,
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/psrain="657BL/63"
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Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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Mus musculus (house mouse)
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Kawai, J., Shinagawa, A., Shibata, K., Yoshino, M., Itch, M., Ishii, Y., Arakawa, T., Hara, A., Fukunishi, Y., Konno, H., Adachi, J., Fukuda, S., Arakawa, M., Ishi, K., Isawa, H., Kondo, S., Yamanaka, I., Saito, T., Saito, T., Gojobori, T., Bono, H., Kasukawa, T., Saito, R., Kadota, K., Matsuda, H., Ashburner, M., Batalov, S., Casavant, T., Fleischmann, W., Gasterland, T., Gissi, C., King, B., Kochiwa, H., Kuehl, P., Lewis, S., Matsuo, Y., Nikaldo, I., Rosole, G., King, H., Kochiwa, H., Wagner, L., Washlo, T., Satai, K., Okido, T., Furuno, M., Aono, H., Baldarelli, R., Barsh, G., Blake, J., Boffelli, D., Bolinga, N., Fletcher, C., Fujita, M., Gariboldi, M., Gustincich, S., Hill, D., Hofmann, M., Hume, D.A., Kamiya, M., Lee, N. H., Lyons, P., Nordone, P., Ring, B., Ringwald, M., Rodriguez, I., Sakamoto, M., Sasaki, H., Sato, K., Schonbach, C., Seya, T., Shibata, Y., Storch, K.F., Suzuki, H., Toyo-oka, K., Wang, K.H., Weitz, C., Whittaker, C., Wilming, L., Massiniah, Y., Massagawa, Y., Kawaji, H., Kohtsuki, S. and Hayashizah, Y. Yoshida, K., Hasegawa, Y., Kawaji, H., Kohtsuki, S. Functional annotation of a full-length mouse cDNA collection
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Mus musculus 7 days neonate cerebellum cDNA, RIKEN full-length enriched library, clone:A730022G11 product:platelet-derived growth factor, C polypeptide, full insert sequence.
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                      GTTGCCCTGGACAAAATACATGTATNTCCATCCCGGAATGGTGCTAGAGTTGGATTAAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Mus musculus"
/mol type="mRNA"
/strain="C57BL/6J"
/db_xref="FANTOM DB:A730022G11"
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/db_xref="taxon:10090"
/tissue_type="cerebellum"
/tissue_type="cerebellum"
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                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (16-UUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research (RIKEN), Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.go.jp, URL.http://genome-gsc.riken.go.jp, Tel:81-45-503-9222, Fax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to
                                                              Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,70 full-length cDNAs
Nature 470, 1410, 1563-573 (2002)

6 (bases 1 to 3405)
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Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/
URL:http://fantom.gsc.riken.go.jp/.
Location/Qualifiers
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                                                  Consortium and the RIKEN Genome
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                                                                     AATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGAAA
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Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Series: IRAK Plate: 35 Row: p Column: 20
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 10242384 This clone has the following problem: frame shifted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  231 cececededadadeceredeceedareadeaaaardereereeredegeereereere
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                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2893)
                                                                                                                               Strausberg_R.
Direct Submission
Submission
Submitted (01-MAY-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGACATCTGCCCTGGCCGGCCAGAGACGGACTCAGGCGGAATCCAACCTGAGTAGTA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /tissue type="Mammary tumor metastatized to lung.
MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hulyk, S.W., Hale, S.M.
Martin, R.G., Muzny, D.
                                                                                                                                                                                                                                                                                      NIH-MGC Project URL: http://mgc.nci.nih.gov
Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Gibert Smith, Ph.D.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89;
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Pred. No. 3.7e-135;
L; Mismatches 578; J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequencing Center
Center code: BCM-HGSC
Web site: http://www.hgsc.bcm.tmc.edu/cdna/
Contact: amg@bcm.tmc.edu
Gunaratne, P.H., Garcia, A.M., Lu, X., Huly/
Ycon, V.S., Kowis, C.R., Lawrence, S., Mart:
Richards, S., Gibbs, R.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           42.3%; Scur. No. 3... 68.4%; Pred. No. 3... 17 Mismatches 5...
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/lab host="DH10B"
/note="Vector: pCMV-SPORT6"
597 c 650 g 778 t
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/clone="IMAGE:3660797"
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/strain="CZECH II"
musculus (house mouse)
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Mus musculus, Similar to platelet-derived growth factor, C
polypeptide, clone IMAGE:3660797, mRNA.
BC029099.1 GI:20809107
HTC.
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1 (bases 1 to 999)

11 (bases 1 to 999)

12 (bases 1 to 999)

Nath-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished

Contact: Robert Strausberg, Ph.D. Email: cgapbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL) DNA Sequencing by: Agencourt Bioscience Corporation

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Contact: Robert Strausberg, Ph.D.
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Clone distribution: MGC clone distribution information can found through the I.M.A.G.B. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAMI2833 row, k column: 23
High quality sequence stop: 676.
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/lab host="DHIOB (T1 phage-resistant)"
/clone_line="NGI GAAP SKIA"
/note="Organ: sKin; Vector: pCMV-SPORT6; Site_1: Not1;
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Average insert size 1.5kb. Library constructed by Life Technologies. Note: this is a NCI_CGAP Library."

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 969)
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<u>AAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTATACAGCTGCAC</u>
                                                     ACCTOGTAACTTCTCAGTGTCC--ATAAGGGAAGAACTAAAGAGAACCGATACCA-TTTT
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National Institutes of Health, Mammalian Gene Collection (MGC)
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/mol_type="mRNA"
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Harrington, J.J., Sherf, B., Rundlett, S., Jackson, P.D., Perry, R., Cain, S., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Leventhal, C., Thornton, M., Ramachandran, R., Whittington, J., Lerner, L., Costanzo, D., McBligott, K., Boozer, S., Mays, R., Smith, J. W., Veloso, N., Klika, A., Hess, J., Cothren, K., Lo, K., Offenbacher, J., Danzig, J. and Ducar, M. Creation of genome-wide protein expression libraries using random activation of gene expression
Nat. Biotechnol. 19 (5), 440-445 (2001)

44115,

Athersys, Inc. 3201 Carnegie Ave, Cleveland, OH 721: 216 431 9900 Fax: 216 361 9596

Contact: Scott J. Cain

21227151

Email: scain@athersys.com High quality sequence stop: 485. Location/Qualifiers

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/organism="Homo sapiens"
/mol type="mRNA"
/db Zref="taxon:9606"
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/note="See 'Creation of Genome-wide Protein Expression
/note="See 'Creation of Genome-wide Protein Expression
Libraries using Random Activation of Gene Expression,
Nature Biotechnology, in press. Note that even though the
cell type indicated is HT1080, since a random activation
method was used, these sequence tags are not necessarily
expressed in HT1080 under normal circumstances."

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Pred. No. 5.4e-115;
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Best Local Similarity 97.8%;
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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811 bp Library Homo

BG185961.1 GI:13707648 RST4916 Athersys RAGE BG185961

Homo sapiens (human) Homo sapiens

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603394005F1 NIH_MGC_90 Homo sapiens cDNA clone IMAGE:5404105 5',
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/mol type="mRNA"
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Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5kb. Library constructed by Life
Technologies Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                                                                                                                  1142 bp mRNA linear EST 01-MAY-2001
602627750F1 NCI_CGAP_Skn4 Homo sapiens cDNA clone IMAGE:4752348 5',
BG681390
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                                                                          ACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCA 1009
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                                                                                            ACCACGAGGTCCTTCAGTTGAGACCAAAGACCGGTGTCAGGGGATTGCACAAATCACTCA 664
                              Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: James Cleaver, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://image.lln.gov
Plate: LiAMloGlO row: d column: 13

High quality sequence stop: 803.
                                                                                                                                                                  CAATTCACAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTG
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1142)
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Pred. No. 1.3e-113;
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ilarity 96.3%;
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Contact: Robert Strausberg, Ph.D.

Email: cgapbs-remail.nih.gov
   Tissue Procurement: Dr. Eliot Spindel
   CDNA Library Preparation: CLONTECH
   CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
   DNA Sequencing by: Agencourt Bioscience Corporation
   Clone distribution: NCI-CGAP clone distribution information can be
   found through the I.M.A.G.E. Consortium/LLNL at:
   http://image.llnl.gov
   plate: LLCM3156 row: 1 column: 14
   High quality sequence stop: 590.
   High quality sequence stop: 590.
   I. 769
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/ste_2: Sfi I; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.0-4:0 Nb. Tissue pooled from
pre-pubertal, post pubertal sn menopausal monkeys.
Constructed by Clontech, Note: this is a NICHD Library."
                                                                                                                                                                                                                                                                                                                                                                           CB309471 AGENCOURT 11834776 NICHD Rh Ov1 Macaca mulatta cDNA clone IMAGE:6893055 5', mRNA sequence.
                                                           1384 TCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAACTGTG 1443
658 GTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGCTGGGT 717
                                                                                          CTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTGTTTTGGAAG 728
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Macaca mulatta
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Cercopithecidae,
Cercopithecinae, Macaca.
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CB309471.1 GI:28832181
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                           Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: LLAM12030 row: i column: 02
High quality sequence stop: 791.
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Pred. No. 2.3e-109;
0; Mismatches 11; 1
      DNA Sequencing by: Incyte Genomics, Inc
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/tissue type="Chondrosarcoma"
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/clone lib="NCI CGAP EDI"
/clone lib="NCI CGAP EDI"
/clone lib="NCI CGAP EDI"
/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac
/phrancial with a modified polylinker; Site_1: EcoR I;
Site_2: Not I; NCI CGAP EDI is a normalized cDNA library
containing the following tissue(s): Chondrosarcoma cell
line CSS: The library was constructed according to Bonaldo
.Lemnon and Soares, Genome Research, 6:791-806, 1996.
First strand cDNA synthesis was primed with an oligo-dT
primer containing a Not I site. Double stranded cDNA was
ligated to an EcoR I adaptor, digested with Not I, and
cloned directionally into pT7T7-Pac vector: The
oligonicleotide used to prime the synthesis of
first-strand cDNA contains a library tag sequence that is
located between the Not I site and the (dT)18 tail. The
sequence tag for this library is GCTCRAGGCT:
TAG LIB=UI-H-EDI
TAG TISSUE=chondrosarcoma
TAG SESC-CGTCAGGCT"
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UI-H-EDI-axw-j-04-0-UI.s1 NCI_CGAP_ED1 Homo sapiens cDNA clone
IMAGE:5834595 3', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                            GAGACCAAAGACCGGIGICAGGGGATIGCACAAAICACTCACCGACGIGGCCCTGGAGCA 1028
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jose Mercuende
cDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
POLYA=Yes.
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I (bases 1 to 686)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                          ACCTCGTAACTTCTCAGTATCCATAAGGGAAGAACTAAAGAGAACCGATACCATTTCTG
                                                                                                                                                                                    243 GCCAGGTTGTTCTCCTGGTTAAACGCTGTGGAGGAACTGTGCCTGTTGTCTCCACAATTG
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                                                                                                                                                   GCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTCTCCCACAATTG
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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RESULT 13 BQ015321/c DEFINITION

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ORGANISM ACCESSION VERSION KEYWORDS SOURCE

REFERENCE AUTHORS TITLE

JOURNAL COMMENT

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FEATURES

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RS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishi, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katch, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Nakamira, M., Nishi, K., Nomura, K., Nuwazaki, R., Ohno, M., Ohasto, N., Okazaki, Y., Saito, R., Satto, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Takeda, Y., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue type="head"
/clone_lib="RIKEN full-length enriched mouse cDNA library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.
Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.
Please visit our web site for further details.
URL:http://genome.gsc.riken.go.jp/.
URL:http://fantom.gsc.riken.go.jp/.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIREN), Laboratory for Genome Exploratory Research (RIREN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (SCC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanaqawa 230-0045, Japan (B-mail:genome-res@gsc.riken.go.jp, WRL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Pax:81-45-503-9216)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
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Pred. No. 5.5e-93;
0; Mismatches 147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /organism="Mus musculus"
/mol_type="mRNA"
/strain="C57BL/61"
/db_xref="FANYOM_DB:C130008P20"
/db_xref="taxon:1009"
/clone="C130008P20"
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of 60,770 full-length cDNAs Nature 420, 563-573 (2002) 6 (bases 1 to 2502) Adachi,J., Aizawa,K., Akimu
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al Similarity 79.3%;
789; Conservative
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                                                                                                                                                              Mus musculus 16 days embryo head cDNA, RIKBN full-length enriched library, clone:Cl30008P20 product:platelet-derived growth factor, C polypeptide, full insert sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsunoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yonaka,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKEN integrated sequence analysis (RISA) system-384-format sequencing pipeline with 384 multicapillary sequencer
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Analysis of the mouse transcriptome based on functional annotation
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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Nature 409 (6821), 685-690 (2001)
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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HTC; CAP trapper.
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/note="vector: pCNV-SPORT6; Library is oligo-dT primed and directionally clones Library is oligo-dT primed and directionally cloned (ErocR site is destroyed upon cloning).
/dredinonally clones insert size 1.7 kb, insert size range 1.2-3; kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 027. Note: this is a NIH MGC Library.

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http://image.llnl.gov
plate: LLAM11538 row: k column:
High quality sequence start: 26
High quality sequence stop: 762.
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Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
                                                                                                                                                                                                                                                            GGAAATCATATCAGGATAAGATTTGTATCTGATGAGTATTTTCCATCTGAACCGGGATTC
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Email: cgapbs-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at:
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KEYWORDS
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AUTHORS
TITLE
JOURNAL
COMMENT
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1 MSLFGLLLVTSALAGQRRGT......DVALEHHEECDCVCRGSTGG
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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Human VEGF-X prote
Human VEGF-X prote
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Human PRO713 prote
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Human growth facto
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AAB03003
AAB10640
AAB10641
                 AAB10651
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ALIGNMENTS

AAY84557 standard; Protein; 345 AA

Amino acid sequence of platelet-derived growth factor C (PDGF-C)

Platelet-derived growth factor C; PDGP-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroplast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling

99WO-US22668

98US-0102461. 98US-0108109. 98US-0110749. 98US-0113002.

INST CANCER RES

transgenic animal; platelet derived growth factor C; PDGF-C;

cardiac hypertrophy; fibrosis.

platelet-derived growth factor (PDGF-C) protein.

Human

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The present sequence represents human platelet-derived growth factor (PDGF-C) (formally designated VEGF-F). PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor.

DGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals comprising PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The puge C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and also be used to promote fibroblast mitogenesis in a mammal and to induce PDGF alpha receptor activation.

Expressing PDGF-C in a mammal. Specific types of human tumours, e.g. choricarcinoma, Wilms tumour, megakaryoblastic leukaemia, lung carcinoma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and erythroleukemia, can be identified by testing for expression of PDGF-C. PDGF-C antagonists can also be used to inhibit tissue remodelling during invasion of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions, especially found in the lung, kidney or liver.
                                                                                                                                                             Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C
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                                         Lee X, Ponten A,
Betsholz C;
(UYHE-) UNIV HELSINKI LICENSING LID
                                                                                                                                                                                                                                             Claim 27; Fig 2; 135pp; English.
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Best Local Similarity 100.
Matches 345; Conservative
                                      Eriksson U, Aase K,
Oestman A, Heldin C,
                                                                                                   WPI; 2000-292954/25.
N-PSDB; AAA12523.
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The patent discloses a method for producing a transgenic, non-human animal over-expressing a platelet derived growth factor C (PDGF-C), or its functional fragment or analogue. The method involves introducing a transgenic PDGF-C DM into a cell of a non-human animal, introducing the cell into a non-human animal and allowing the cell to develop into a managenic, non-human animal. The transgenic animal is useful as a model to study disease tattes characterised by over-expression of PDGF-C and to find therapy for those diseases, particularly hypertrophy and interior in various organs including the heart. The present sequence

is PDGF-C protein from human.

A transgenic animal over-expressing platelet derived growth factor C useful to study and find therapy for disease associated with PDGF-C over-expression, including cardiac hypertrophy and fibrosis

Disclosure; Page 40-42; 48pp; English

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Aase K,

Ponten A,

Li X,

WPI; 2002-010700/01.

(LUDW-) LUDWIG INST CANCER RES

28-MAR-2001; 2001WO-US09855. 28-MAR-2000; 2000US-192507P.

WO200172132-A1. Homo sapiens

04-OCT-2001

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LIEBVRLYSCIPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                          LIBEVELYSCTPENDESVSIREELKRIDIIEWPGCLLVKRCGGNCACCLHNCNSCQCVPSK 300
                                                                      LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
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Best Local Similarity 100.0
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RESULT 3
AAY33679
ID AAY3

AAE13212 standard; Protein; 345

(first entry)

12-FEB-2002

AAE13212

RESULT 2
AAE13212
ID AAE1
XX
AC AAE1
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DT 12-FI

AAY33679 standard; Protein; 345 AA.

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has tranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially by mammals. Especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially can be used to treat cardiac hypertrophy contact or treat angiogenic treat angiogenic treat angiogenic disorders in mammals (especially humans) e.g. cancer or screen for antagonists and agonists, and the antagonists administered to carteat angiogenic disorders in mammals (especially humans) e.g. cancer or segent therapeutically as antagonists, as above. VEGF-E can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful therapeutically as antagonists, as above. The antibodies are also cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation) by contacting the antibody with a tissue sample and detecting formation. WEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E gene expression in tissue samples. They can also be used to disquose a disease or susceptibility to a disease related to a mutated form of VEGF-E can a mutation in the VEGF-E-encoding sequence isolated from a sample. They may also be used to produce probes useful to detect related sequences or for gene mapping. This sequence probes useful to detect related sequences or for gene mapping. This invention.
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                                                                                                                                  VEGF-E; human; vascular endothelial cell growth factor; wound repair; treatment; cardiovascular disorder; endothelial disorder; therapy; tissue generation; regeneration; cardiac hypertrophy; cancer; detection; angiogenic disorder; age-related macular degeneration; vascular disease; neovascularization; tumor; gene mapping.
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                                                                                                                                                                                                                                                                                                                                                                       99WO-US05190,
                                                                                                                                                                                                                                                                                                                                                                                                          98US-0040220.
                                                        11-JAN-2000 (first entry)
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Matches 343; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GETH ) GENENTECH INC.
                                                                                             Human VEGF-E protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1999-580306/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ferrara N, Kuo SS;
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1 MSLFGLLLVTSALAGORRGTQAESNLSSKFOFSSNKEQNGVODPQHERIITVSTNGSIHS

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PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEFSDGTIL 120
                                                         LPLDLLINNALTAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240
                                                                                                                                LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                   241 LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                                           Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein.
PRFPHTYPRNTVLVMRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL
                                          GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
                                                                                                     301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                                                                                                             VIKKYHEVLOLRPKTGVRGLHKSLIDVALEHHEECDCVCRGSIGG 345
                                                                                                                                                                                                                                                      AAY41766 standard; Protein; 345 AA.
                                                                                                                                                                                                                                                                                                                      Human PRO200 protein sequence.
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98US-0040220,
98US-0078886,
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9803-0078936.
9803-0078939.
9803-0079294.
9803-0079663.
9803-0079669.
9803-0079689.
9803-0079728.
9803-0079728.
9803-0079929.
9803-0080105.
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98US-0077649.
98US-0077791.
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                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
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20-MAR-1998;
20-MAR-1998;
20-MAR-1998;
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12-MAR-1998;
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27-MAR-1998;
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01-APR-1998;
08-APR-1998;
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17-MAR-1998;
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PRFPHTYPRNITYLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEVEBFDGTL 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PREPHTYPRINTVLVWRLVAVBENVWIQLTFDERFGLEDPEDDICKYDFVEVEPSEDGTIL 120
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The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagulation disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AA233891 to AA234338, and AAY41685 to AA441774 represent polynucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                   MSLFGLLLVTSALAGORRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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                                                                                                                                                                                                                                                                                                                                       Query Match 99.6%; Score 1851; DB 20; Length 345; Best Local Similarity 99.4%; Pred. No. 7e-179; Matches 343; Conservative 2; Mismatches 0; Indels 0
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98US-0072635.
98US-0088089.
98US-0090544.
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05-JUN-1998
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                                                                                                                                                                                                                                                 invention.
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                        9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081195-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-0081106-9805-
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N-PSDB; AAZ34296.
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22-APR-1998;
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23-APR-1998;
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22-MAY-1998;
22-MAY-1998;
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06-MAY-1998;
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Growth factor homologs and the nucleic acids that encode them, e.g. for treating liver damage, ischemia, multiple sclerosis ar

e.g. for treating li Alzheimer's disease

Sheppard PO, Gilbertson DG;

03-MAY-2000; 2000WO-US40047.

10-NOV-1999; 99US-0164463. 04-FEB-2000; 2000US-0180169.

(ZYMO) ZYMOGENETICS INC. Hart CE,

WPI; 2000-687541/67.

Gilbert T,

N-PSDB; AAC81582

99US-0304216

03-MAY-1999;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; zvegf3; zvegf4 fusion; growth factor homologue; VEGF/PDGF family; CUB domain; PDGF-like activity; mitogenic; osteogenic; neovascularisation; tissue repair; proliferation; differentiation; liver damage; neuroregenerative; Alzheimer's disease; multiple sclerosis; periodontal disease; bone fracture; wound healing; vulnerary; ischaemia;
                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                             1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                       MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                         The present sequence represents a vascular endothelial growth factor related (WBGF-R) protein. VBGF-R can be used in assays to identify compounds that bind to it or that annagonize its activity. VBGF-R antagonists (e.g. anti-VBGF-R antibodies) are useful for inhibiting tissue growth. This is useful for inhibiting tumour growth and for treating cancer. VBGF-R itself can be used to stimulate tissue growth, anglogenesis and to treat coronary artery blockage. The VBGF-R coding sequence can be used for the recombinant production of the VBGF-R protein.
                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                        growth factor related protein and related for identifying antagonists and binding
                                                                                                                                                                                                                                                                                                                                                      ;
0
                                                                                                                                                                                                                                                                                                                         Length 345;
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                                                                                                                                                                                                                                                                                                                     Score 1851; DB 20;
Pred. No. 7e-179;
2; Mismatches 0;
                                                                                                                Claim 1; Page 56-58; 62pp; English
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                                                                                                                                                                                                                                                                                                                   99.6%;
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                                                                                                                                                                                                                                                                                                                                    Best_Local Similarity 99.4
Matches 343; Conservative
                                             . vascular endothelial
polynucleotide, useful
compounds
               1999-458680/38
                                                                                                                                                                                                                                                                                           345 AA;
                            N-PSDB; AAX86352
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                                                                                                                                                                                                                                                                                           Sequence
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                                                                                                                                                                                                                                                                                                                      Query Match
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09-NOV-2000

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The invention relates to the human growth factor homologue zvegf4

(AAB48653), and nucleic acids encoding it (AAC81555). Zvegf4 is a member

of the PDGF (platelet-derived growth factor)/VBGF (vascular endothelial

growth factor) family. Zvegf4 has a growth factor domain (AAB48654)

contracterised by a PDGF cystine knot structure, and a CUB domain

contracterised by a PDGF cystine knot structure, zvegf4 has PDGF-like

activity, having mitogenic activity on fibroblasts, vascular smooth

contracted the same period activity on fibroblasts, vascular smooth

contracted acids, the recombinant expression of human zvegf4/human zvegf4

contracted acids, the recombinant expression of human zvegf4/human zvegf4 or fragments thereof, particularly human zvegf4/human zvegf4 or a fragment thereof; a method of activating

contracted acids, the recombinant expression of human zvegf4, an antibody

contracted acids, the recombinant expression of human zvegf4, an antibody

contracted acids, the recombinant expression of human zvegf4, an antibody

contracted acids, the receptor using a zvegf4-derived polypeptide; a

cell-surface PDGF receptor using a zvegf4-derived polypeptide; a

cell-surface PDGF receptor using a zvegf4-derived polypeptide; a

confliction of modulating the proliferation, differentiation, migration or

confliction of modulating the proliferation. They are particularly used for

conflicting the properties; and a method of detecting a genetic

collular differentiation or proliferation. They are particularly used for

collular differentiation or proliferation. They are particularly used for

collular differentiation or proliferation or modulate neuritie growth (e.g., in the treatment of periodontal disease and fractures. They may be used

consedito enhance expansion and mobilisation of haemacopoietic stem cells

cused to enhance expansion and mobilisation of haemacopoietic stem cells

cunductured of scheme and an endothelial precursor stem cells, which may be used to

conduct the present sequence represents human zvegf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 GRWCGSGTVPGKQISKGNQIRIRFVSDBYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 48; Page 125-126; 143pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
Matches 343; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             345 AA;
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LPLDLLANNATTAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNL
                181 LPLDLLANAITAFSTLEDLIRYLEBERWQLDLEDLYRPTWQLLGGKAFVPGRKSRVVDLNL
                                                        241 LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
                                                                                                                                                                                                                                                                                                                                       Human, secreted protein; transmembrane protein, PRO; EST; cytostatic; expressed sequence tag; detection; cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KP, Botstein D, Desnoyers L, Eaton DL;
E, Fong S, Gao W, Gerber H, Gerriteen ME;
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel PRO polypeptides and polynucleotides used in detection metleto target bioactive molecules to specific cells, and to modulate
                                                                                                                                  301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG
                                                                                                                                                                                                                                                                                                             Human PRO200 (UNQ174) protein sequence SEQ ID NO:488.
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                                                                                                                                                                                                                          AAB44322 standard; Protein; 345
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99US-0126773.
99US-0130232.
99US-0131445.
99US-0134287.
99US-0141037.
99US-0145698.
99US-0145698.
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2000WO-US00277.
2000WO-US00376.
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lvaroff E,
                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Filvaroff
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cellular activities -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18-FEB-2000;
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30-NOV-1999;
02-DEC-1999;
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16-DEC-1999;
30-DEC-1999;
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06-JAN-2000;
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Goddard A,
Kljavin IJ,
                                                                                                                                                                                                                                                                                    08-FEB-2001
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26-JUL-1999
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                                                                                                                                                                                                            AAB44322
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       LIBEVRLYSCTPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention describes a method for enhancing tissue growth, promoting wound healing or stimulating smooth muscle growth by administering a platelet-derived growth factor (PDGF) related protein, designated LPB or its analogue. Also described is a method of slowing the progress of atherosclerosis or treating atherosclerosis comprising the administration of an LPB antagonist. The method is useful for enhancing tissue growth, promoting wound healing and stimulating smooth muscle growth. Antagonists of LPB are useful for treating atherosclerosis. The present sequence represents human LPB, which is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Enhancing tissue growth and promoting wound healing by administering platelet-derived growth factor related protein, LPB or its analog and treating atherosclerosis by administering LPB antagonist
                                                                                                                                                                                                                                                     Human, platelet derived growth factor related protein, LPB, VEGFh, vascular endothelial growth factor h; tissue regeneration; vulnerary; atherosclerosis; PDGF-related protein; antiarteriosclerotic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                     301 VIKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                   VIKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Indels
                                                                                                                                                                                                                           Human platelet-derived growth factor related protein LP8.
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Pred. No. 7e-179;
2; Mismatches C
                                                                                                                                        AAB24250 standard; Protein; 345 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99.6%;
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                                                                                                                                                                                                   (first entry)
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les 343; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          also called VEGFh.
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                                                                                                                                                                                                                                                                                                                    Homo sapiens
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            241
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activity. The polynucleotides and polypeptides can be used for detecting molecules to RRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting targeting the polypeptide target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC7807 represent PCR primers and probes used in the isolation of the PRO polynucleotide sequences.
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                                                                                                                                                    Score 1851; DB 21;
Pred. No. 7e-179;
2; Mismatches 0;
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This invention describes a novel vascular endothelial growth factor-X (VBGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipporiatic and antidiabetic activity and acts as an anglogenesis and vascularization cautidiabetic activity and acts as an anglogenesis and vascularization of requirementary career, rheumatoid arthritis, psoriasts and diabetic retinopathy by inhibiting anglogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote SKAIN graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration. This sequence represents the RACE generated human VEGF-X protein described in the method of the invention.
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4atches 343; Conservative
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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polymucleotide (IIa) which has vulnerary, cytostatic, antiheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood and tissue repeneration and organ and tissue repeneration and organ and tissue repeneration and organ for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote
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99US-0164131.
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                                                                                                                                                                                                                                              VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; antirheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; andiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
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301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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Pred. No. 7e-179;
2; Mismatches 0;
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                                                                                              AAB10644 standard; Protein; 345
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99US-0164131.
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11 Similarity 99.4%;
343; Conservative
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                                                                                                                                                                                                            Human VEGF-X protein #4.
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N-PSDB; AAA71990.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antipsoriatic and antidiabetic activity and acts as an angiogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic estinopathy by inhibiting angiogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ and tissue repair in a subject. The products of the invention are useful
PRFPHTYPRNTVLVWRLVAVBENVWIQLIFDERFGLEDPEDDICKYDFVEVEBPSDGTIL 120
                                                                                                                                                                        LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                                                                                      VEGF-X; vascular endothelial growth factor; human; vulnerary; cytostatic; anticheumatic; antiarthritic; antipsoriatic; antidiabetic; treatment; angiogenesis regulator; vascularization regulator; cancer; psoriasis; rheumatoid arthritis; diabetic retinopathy; blood vessel; organ repair; tissue regeneration; tissue repair; wound; dermal ulcer; pressure sore; venous sore; diabetic ulcer; burns; skin graft growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New vascular endothelial growth factor protein, useful for treating or preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
              PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL
                                                                   GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
                                                GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA
                                                                                                LPLDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNL
                                                                                                                      181 LPLDLINNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNI
                                                                                                                                               LIBEVRLYSCIPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK
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for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graft growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human 990126vegx protein used to illustrate the method of the invention.
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Pred. No. 7e-179;
2; Mismatches 0;
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08-NOV-1999;
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Homo sapiens

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This invention describes a novel vascular endothelial growth factor-X (VEGF-X) protein (Ia) and its encoding polynucleotide (IIa) which has vulnerary, cytostatic, antirheumatic, antiarthritic, antigoriatic and antidiabetic activity and acts as an anglogenesis and vascularization regulator. An antisense molecule of the invention is useful for treating or preventing cancer, rheumatoid arthritis, psoriasis and diabetic retinopathy by inhibiting anglogenic activity or inappropriate vascularization including formation and proliferation of new blood vessels, growth and development of tissues, tissue regeneration and organ at the state growth, as subject. The products of the invention are useful for preparing medicaments for treating wounds such as dermal ulcers, pressure sores, venous sores, diabetic ulcers and burns and to promote skin graff growth, tissue repair, proliferation of new blood vessels, tissue regeneration and organ repair, proliferation of new blood vessels, tissue regeneration and organ repair by promoting angiogenic activity or vascularization. This sequence represents the human VEGF-X protein
                                                         preventing diseases associated with inappropriate angiogenesis activity such as cancer, rheumatoid arthritis, psoriasis and wounds -
                           growth factor protein, useful for treating
                                                                                                                                          Claim 72; Fig 12; 127pp; English.
                           New vascular endothelial
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MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60 1 MSLFGLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60 ö Score 1851; DB 21; Length 345; Pred. No. 7e-179; 2; Mismatches 0; Indels 0 Query Match
Best Local Similarity 99.4%;
Matches 343; Conservative g

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AAB19578 standard; Protein; 345 AA AAB19578;

(first entry) 22-JAN-2001 Human PRO200 (vascular endothelial growth factor E).

ocular disease; refinopathy; maculopathy; therapy; retinitis pigmentosa; macular degeneration; retinal detachment; retinal tear; macular hole; myopla; traumatic chorioretinopathy; acute retinal necrosis syndrome; contusion; dedma; retinal vision occlusion; vascular disease; retinal vasculitis; thrombocytopenic purpura; uveitis; retinal occlusion. PRO200; vascular epithelial growth factor E; VEGF-E; human;

Henzel WJ, Wood WI; 25..29 /note= "Asn is N-glycosylated" 'note= "Asn is N-glycosylated" note= "Asn is N-glycosylated" Gurney AL, Hebert C, Kuo SS, La Fleur M, 282..288 /note= "N-myristoylation" 319..325 "N-myristoylation" 'note= "N-myristoylation" "N-myristoylation" "N-myristoylation" /label= Signal_peptide /label= Mature_Pro200 Location/Qualifiers /note= "Amidation" 10-MAR-2000; 2000WO-US06319. 99US-0123957. ..133 ..123 254..258 281..287 55..59 /note= /note= /note= Goddard A, Kljavin IJ, (GETH) GENENTECH INC WO200053760-A2 Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site Modified-site 12-MAR-1999; 14-SEP-2000 Perrara N, Klein RD, Key Peptide Protein

cells Novel PRO polypeptides useful for preventing or rescuing retinal cel from injury caused by ocular diseases such as retinitis pigmentosa, retinopathy, retinal degenerative diseases, degenerative myopia, WPI; 2000-587437/55. N-PSDB; AAA88515

Kabakoff RC;

Claim 2; Fig 2; 140pp; English.

uveitis

The present sequence is that of human PRO200 or vascular endothelial growth factor E (VEGF-E), as predicted from a cDNA clone (see AAA88515) that was isolated from a glioma cell line G61.

Clone (see AAA88515) that showed homology to VEGF. PRO200 has a predicted mol.wt. of 39,029 and a pl of about 6.06. A method for producing PRO polypeptides, including PRO200, using a host cell transformed with a vector comprising a PRO nucleic acid is claimed. The invention relates to the use of PRO polypeptides to delay, the invention relates to the use of PRO polypeptides to delay. The invention relates to the use of PRO polypeptides to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal again or cells, amarcine cells, displaced amacrine cells, including Mueller cells and pipolar neurons, and supportive cells (including Mueller cells and pipolar neurons, and supportive cells (including Mueller cells and cells are preferably photoreceptors and aphotoreceptor cell injury or by an ocular disease selected from retinal detachment, retinal cells including age-related, retinal decamental reamma or by an ocular disease selected from retinal decamental retinal degenerative myopia, acute retinal neorosis syndrome, traumatic chorioretinopathies or contusion such as Purtscher's retinopathy, celmal injury, lagin or conditions such as central or branch retinal vision collagen vascular alseases, thrombocyclopenic purpura, uveits, retinal vasculitis and occlusion associated with Eales

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sequences given in the exemplification of the present invention.
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Best Local Similarity
Matches 343; Conserv
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 Human, immune related disease; diagnosis; antiinflammatory; cardiant; dermatological; antiarthritic; antirheumatic; immunosuppressive; haemostatic; antiarthritic; antirheumatic; immunosuppreceive; matianaemic; hepatotropic; virucide; antipsoriatic; antialergic; antiathaetic; systemic lupus erythematosus; rheumatoid arthritis; antiathaetic; systemic lupus erythematosus; rheumatoid arthritis; wostecarthritis; spondyloarthropathy; systemic sclerosis; asronidosis; didopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis; systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus; autoimmune thrombocytopaenia; immune-mediated renal disease; inflammatory bowel disease; julten-sensitive enteropathy; autoimmune disease; immune-mediated skin disease; immunological disease; immuno-mediated skin disease; allergic disease; mimmunological disease; imto-mediated skin disease; allergic disease; we graft rejection; graft-versus-host-disease.
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                                                                                                                                                       PRFPHTYPRNTVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
                                                                                                                                                                                                    GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                                                                                                                       PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEBPSDGTIL 120
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                                                                                            1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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                                              Length 345;
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                                            Score 1851; DB 21; Length
Pred. No. 7e-179;
2; Mismatches 0; Indels
disease and systemic lupus erythematosus (claimed).
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99US-0123957.
99US-0125775.
99US-0128849.
99WO-US08615.
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                                          Query Match
Best Local Similarity 99.4
Matches 343, Conservative
                       345 AA;
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12-MAR-1999;
23-MAR-1999;
12-APR-1999;
20-APR-1999;
28-APR-1999;
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The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO antibodies, agonists and antagonists are useful for treating and disgnosing immune related disorders. The disorders are selected from systemic lupus erythematosus, rheumatoid arthritis, osteoarthritis, juvenile chronic arthritis, spondyloarthropathies, systemic solerosis, idiopathic inflammatory myopathies, systemic vasculitis, sarcoidosis, autoimmune haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes mellitus, immune-mediated renal disease, demyelinating diseases of the central and peripheral nervous systems, hepatobiliary diseases of the central and peripheral nervous systems, demyelinating diseases of the central control disease, gluten-sensitive enteropathy and whipple's disease, immunological diseases of the lung, and transplantation associated diseases including graft rejection and graft-versus-host-disease.

MACSB397 to AACSB398 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AACSB599 to AACSB642 and AABB34414 to AAASB477 represent human PRO polynucleotide and protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus
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on Di, Smith V;
Yan M;
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Pan J, Pennica D, Shelton I
, Watanabe CK, Wood WI, Yar
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Kabakoff RC, Lu Y, Pan S
Stewart TA, Tumas D, Wat
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Gaps

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99.6%; Score 1851; DB 21; Length 345; larity 99.4%; Pred. No. 7e-179; Conservative 2; Mismatches 0; Indels 0

345 AA;

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      1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQESSNKEQNGVODPQHERIITVSTNGSIHS 60

      Db
      1 MSLFGLLLTSALAGGRGGTGAESNLSSKFQESSNKEQNGVODPQHERIITVSTNGSIHS 60

      Qy
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      Db
      61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEBEDGGTIL 120

      Qy
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      Db
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      Qy
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      Qy
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      Qy
      301 VTKKYHEVLOLRPRYGCHKSLTDVALEHHEBCDCVCRGSTGG 345
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Search completed: November 25, 2003, 21:02:13 Job time : 36.9375 secs

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Sequence 3, Appli
Sequence 32, Appli
Sequence 3, Appli
Sequence 2, Appli
Sequence 4, Appli
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                                                                                                                                                              November 25, 2003, 21:04:39; Search time 24.3006 Seconds (without alignments) 2618.575 Million cell updates/sec
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1 MSLFGLLLVTSALAGQRRGT......DVALBHHEECDCVCRGSTGG 345
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US-09-95-4

US-09-78-695-48

US-09-78-697-488

US-09-978-192A-488

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GenCore version (c) 1993 - 2003
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Listing first 45 summaries
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Gapop 10.0 , Gapext 0.5
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No.
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APPLICANT: ERIKSSON, UIF
APPLICANT: ENERSON, UIF
APPLICANT: EVERESON, UIF
APPLICANT: POWIEN, Annica
APPLICANT: ASSE, Karin
APPLICANT: ASSE, Karin
APPLICANT: LI, Hong
TITLE OF INVENTION: NON-HUMAN TRANSGENIC ANIMALS EXPRESSING PLATELET-DERIVED GROWTH
TITLE OF INVENTION: (PDGF-C) AND USES THEREOF
FILE REFERENCE: 1064/48487
CURRENT APPLICATION NUMBER: US/09/818,943
CURRENT FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 60/192,507
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATCHTIN VERSION 3:0
SEQ ID NO 1
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100.0%; Score 1858; DB 9;
Best Local Similarity 100.0%; Pred. No. 3.1e-179;
Matches 345; Conservative 0; Mismatches 0;
US-09-978-585A-488
US-09-978-191A-488
US-09-978-564A-488
US-09-918-564A-488
US-09-918-533A-488
US-09-918-533A-488
US-09-918-53A-488
US-09-918-53A-488
US-09-918-423A-488
US-09-978-123A-488
US-09-978-187A-488
US-09-978-187A-488
US-09-978-187A-488
US-09-978-187A-488
US-09-978-187A-488
US-09-978-187A-488
US-09-978-187A-488
US-09-978-188A-488
US-10-140-018-286
US-10-140-018-286
US-10-140-024-286
US-10-140-978-186
US-10-140-978-186
US-10-140-978-186
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US-10-140-978-286
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US-10-140-978-286
US-10-140-926-286
US-10-141-698-286
US-10-141-698-286
US-10-141-702-286
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       TYPE: PRT
ORGANISM: Homo sapiens
US-09-818-943-1
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61 PRFPHTYPRNITVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEVEFSBGTIL 120 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180

PRFPHTYPRINTVLVMRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEREPSDGTIL

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MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS

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241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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                                                                                                                         301 VTKKYHEVLOLRPKTGVRGLHKSLTDVALEHHBECDCVCRGSTGG 345
                                                                                          301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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US-10-086-623-32
                                                                                                                                                                                                                                                Sequence 32, Application US/10086623
Publication No. US20020164710A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                              APPLICANT: BRIKSSON, U1f
APPLICANT: AASE, Karin
APPLICANT: LI, Kuri
APPLICANT: POWTEN, Annica
APPLICANT: UUTELA, MARKO
APPLICANT: ALITALO, Kari
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ORGANISM: Homo sapiens
                                                                                                                                                                                                          RESULT 3
US-10-086-623-32
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                                                                                                   241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                         LPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240
                                                                                                                                                               LIBEVRLYSCIPRNFSVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                            121 GRWCGSGTVPGKQISKGNQIRIRFVSDBYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
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                                                                                                                                                                                                                                                                                 301 VTKKYYHEVLQLRPKTGVRGLHKSLTDVALEHHBECDCVCRGSTGG 345
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APPLICANT: ALITALO, KARTI
APPLICANT: BELDIAN, ARTHER
APPLICANT: HELDIN, CArl-Henrik
APPLICANT: HELDIN, CArl-Henrik
APPLICANT: HELDIN, CArl-Henrik
APPLICANT: HERENCYZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REPRENCE: 09-410349-ERikeson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209A
CURRENT APPLICATION NUMBER: 09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOUTWARE: PATCHTIN OF: 2.0
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Best Local Similarity 100.0
Matches 345; Conservative
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UUTELA, Marko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: ERIKSSON, Ulf
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LEE, Xuri
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No. US20020164
GENERAL INFORMATION:
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US-09-852-209A-3
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LENGTH: 345
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APPLICANT:
APPLICANT:
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APPLICANT: OESTWAN, ARDER APPLICANT: AREA AREALISAND, AREA APPLICANT: MILLIAND, AREA APPLICANT: HELDIN, CAR1-Henrik
TITILE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES 1
FILE REPERENCE: 1064/448322
CURRENT APPLICATION NUMBER: US 60/107,852
PRIOR APPLICATION NUMBER: US 60/107,852
PRIOR APPLICATION NUMBER: US 60/113,997
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-10-04
PRIOR FILING DATE: 1999-11-0
PRIOR FILING DATE: 1999-11-10
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241 LIEEVRLYSCIPRNESVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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                                                     301 VTKKYHEVLQIRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                           301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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APPLICANT: OUTLAL, MAINO
APPLICANT: OCSTMAN, ARNE
APPLICANT: GESTMAN, ARNE
APPLICANT: HELDIN, CAL'Henrik
APPLICANT: HELDIN, CAL'Henrik
APPLICANT: HELDIN, CAL'Henrik
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TILE OF INVENTION: THEREFOR, AND USES THEREOF
TILE OF INVENTION NUMBER: US/10/131,600
CURRENT APPLICATION NUMBER: US/09/410,349
PRIOR FILING DATE: 1999-09-30
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1998-11-12
PRIOR FILING DATE: 1998-12-13
PRIOR FILING DATE: 1998-12-14
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,02
PRIOR APPLICATION NUMBER: 60/113,02
PRIOR PLING DATE: 1999-05-21
PRIOR PRING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
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100.0%; Pred. No. 3.1e-179;
tive 0; Mismatches 0; ]
                                                                                                                                                                                                                                         Sequence 3, Application US/10131600
Publication No. US20030082670A1
GENBRAL INPORMATION:
APPLICANT: ERIKSSON, UIF
APPLICANT: AASE, Karin
APPLICANT: PONTEN, Annica
APPLICANT: PONTEN, Annica
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 39
SOFTWARE: Patentin Ver. 2.0
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Best Local Similarity 100.1
Matches 345; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; LENGTH: 345
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-131-600-3
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APPLICANT: UUTELA, MARKO

APPLICANT: UUTELA, MARKO

APPLICANT: ALITALO, KATI

APPLICANT: ALITALO, KATI

APPLICANT: CESTWAN, ATTHER

APPLICANT: ALITALO, CALI-HENTIK

TITLE OF INVENTION: PLATELET DERIVED GROWTH FACTOR D, DNA CODING THEREFOR AND USES THE

FILE REFERENCE: 1064/44833C

CURRENT APPLICATION NUMBER: US/10/086,623

PRIOR APPLICATION NUMBER: US 60/107,852

PRIOR APPLICATION NUMBER: US 60/103,997

PRIOR APPLICATION NUMBER: US 60/103,997

PRIOR APPLICATION NUMBER: US 60/150,604

PRIOR APPLICATION NUMBER: US 60/157,108

PRIOR APPLICATION NUMBER: US 60/157,766

PRIOR APPLICATION NUMBER: US 60/157,766

PRIOR PRILING DATE: 1999-10-04

PRIOR PLING DATE: 1999-10-05

PRIOR PRILING DATE: 1999-11-0

PRIOR PRILING DATE: 1990-11-0

PRIOR PRINCE DATE: 1990-11-0

PRINCE PRINCE DATE: 1990-11-0

PRINCE DATE: 1990-
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  241 LIBEVRLYSCTPRNFSVSIRBELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
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                                                                 301 VTKKYHBVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                                          301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: misc feature; OTHER INFORMATION: Amino acid sequence for PDGF-C US-10-260-539-32
                                                                                                                                                                                                                                                        Sequence 32, Application US/10260539
Publication No. US20030073637A1
GENERAL INFORMATION:
APPLICANT: ERIKSSON, UIF
APPLICANT: AASE, Karin
APPLICANT: LI, Xuri
                                                                                                                                                                                                                                                                                                                                                                                                                                    PONTEN, Annica
UUTELA, Marko
ALITALO, Kari
OESTMAN, Arne
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                       Length 345;
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                                                    GENERAL INCORMATION:

APPLICANT: Hart, Charles E.

APPLICANT: Glibertscor, Debra G.

TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE,

TITLE OF INVENTION: LIGAMENT AND CARTILAGE

FILE REFREENCE: 00-12

CURRENT APPLICATION NUMBER: US/09/823,033

CURRENT FILING DATE: 2001-03-29

NUMBER OF SEQ ID NOS: 5

SOFTWARE: FastSEQ for Windows Version 3.0

SEQ ID NO 2

LENGTH: 345
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US-09-923-995-4
; Sequence 4, Application US/09923995
; Patent No. US20020081700A1
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; TITLE OF INVENTION: SNAKE VENOM POLYPEPTIDE ZSNK1
; FILE REFERENCE: 00-47
CURRENT FILING DATE: 2001-08-07
; PRIOR APPLICATION NUMBER: US/09/923,995
; CURRENT FILING DATE: 2001-08-07
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PastSEQ for Windows Version 3.0
; SEQ ID NO 4
; LEGTH: 345
                                                                                                                                                                                                                                                                                                    Query Match 99.6%; Score 1851; DB 9;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0;
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                            Sequence 2, Application US/09823033 Patent No. US20020004225A1
                                                                                                                                                                                                                                         ; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-823-033-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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Best Local Similarity
RESULT 6
US-09-823-033-2
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                                                      1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                          1 MSLFGLLLITSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
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US-09-795-006A-149

i Sequence 149, Application US/09795006A

j Sequence 149, Application US/09795006A

j Patent No. US20020151680A1

j GENERAL INFORMATION:

j APPLICANT Alitalo et al

i TITLE OF INVENTION: MATERIALS AND METHODS INVOLVING HYBRID VASCULAR

i TITLE OF INVENTION: ENDOTHELIAL GROWTH FACTOR DNAS AND PROFEINS

i TITLE OF INVENTION: ENDOTHELIAL GROWTH PACTOR DNAS AND PROFEINS

i CURRENT APPLICATION NUMBER: US/09/795,006A

j RIOR APPLICATION NUMBER: US 60/205,331

j PRIOR APPLICATION NUMBER: US 60/205,331

j PRIOR APPLICATION NUMBER: US 60/185,205

j NUMBER OF SEQ ID NOS: 175

j SEQ ID NO 149

j EBNGTH: 345
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2; Mismatches
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Best Local Similarity 99.4
Matches 343; Conservative
  343; Conservative
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US-09-795-006A-149
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301 VTKKYHEVLOLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                 US-09-978-295A-488
; Sequence 488, Application US/09978295A
; Patent No. US20020156006A1
; GENERAL INFORMATION:
; APPLICANT: Asklenazi, Avi
; APPLICANT: Bakker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
                                                                                                                                                                                        Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
                                                                                                                                                        Gao, Wei-Clang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
                                                                                                                                                                                                                                                               Paoni, Nicholas F.
                                                                                                                              Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
                                                                                                                        Eaton, Dan
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APPLICANT:
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APPLICANT:
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PRIOR APPLICATION NUMBER: 60/07929
PRIOR FILING DATE: 1998-03-25
PRIOR FILING DATE: 1998-03-26
PRIOR PLING DATE: 1998-03-27
PRIOR PLING DATE: 1998-03-37
PRIOR PLING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/08129
PRIOR PLING DATE: 1998-04-01
PR
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121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                       181 LPLDLLNNAITARSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNL 240
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61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEPSDGTIL 120
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CURRENT APPLICATION NUMBER: U5/09/978,697
CURRENT FILING DATE: 2001-10-16
PRIOR PEDICATION NUMBER: U5/09/978,697
PRIOR PEDICATION NUMBER: 06/06220
PRIOR APPLICATION NUMBER: 06/06220
PRIOR APPLICATION NUMBER: 06/06220
PRIOR APPLICATION NUMBER: 06/064249
PRIOR FILING DATE: 1997-11-13
PRIOR PEDICATION NUMBER: 06/06364
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: 60/06364
PRIOR APPLICATION NUMBER: 60/06364
PRIOR PELLING DATE: 1997-11-21
PRIOR PELLING DATE: 1997-11-21
PRIOR PELLING DATE: 1997-11-21
PRIOR PELLING DATE: 1998-03-10
PRIOR PELLING DATE: 1998-03-10
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Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
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Patent No. US20020169284A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
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APPLICATION NUMBER: 60/077641
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Pan, James;
Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Williams, P. Mickey
Wood, William I.
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Kuo, Sophia S.
Napier, Mary A.
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Desnoyers, Luc
Eaton, Dan
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                                                   PRIOR AFFILCATION NUMBER: 60/083495
PRIOR APPLICATION NUMBER: 60/083495
PRIOR APPLICATION NUMBER: 60/083499
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-04-30
PRIOR PLING DATE: 1998-05-07
PRIOR PLING DATE: 1998-05-13
PRIOR PLING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR PRIOR PLING DATE: 1998-05-15
PRIOR PRIOR DATE: 1998-05-15
PRIOR PRIOR DATE: 1998-05-15
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PRIOR PRIOR PRIOR DATE: 1998-05-15
          FILING DATE: 1998-04-28
APPLICATION NUMBER: 60/083392
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Matches 343; Conservative
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	NUMBER: 60/07955 NUMBER: 60/07965 1998-03-25 NUMBER: 60/07966 1998-03-27 NUMBER: 60/07966 1998-03-27 1998-03-27 1998-03-30 1998-03-30 1998-03-30 1998-03-30 1998-03-30 NUMBER: 60/08010 1998-03-30 NUMBER: 60/08010 1998-03-31 NUMBER: 60/08010 1998-03-31 NUMBER: 60/08010 1998-03-31 NUMBER: 60/08013 1998-03-31 NUMBER: 60/08032 1998-03-31 NUMBER: 60/08032 1998-04-01 NUMBER: 60/08032 1998-04-01 NUMBER: 60/080333 1998-04-01 NUMBER: 60/080333 1998-04-01 NUMBER: 60/080333	MBER: 60 9998-04-0 9998-04-0 9998-04-0 9998-04-0 9998-04-0 9988-04-0 9988-04-0 9988-04-0 9988-04-0 9988-04-0 9988-04-0 9988-04-0 9988-04-1
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PRIOR APPLICATION NUMBER: 60/08204
PRIOR APPLICATION NUMBER: 60/08204
PRIOR FILING DATE: 1998-04-22
PRIOR PRICATION NUMBER: 60/082796
PRIOR PRING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-22
PRIOR PELICATION NUMBER: 60/08336
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-23
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-07
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APPLICATION NUMBER: 60/064249
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APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Williams, Daniel
APPLICANT: Wood, Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
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                                                                                                                  Query Match 99.6%; Score 1851; DB 10;
Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0;
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CURRENT APPLICATION NUMBER: US/09/978,192A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
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Sequence 488, Application US/09978192A
Patent No. US202017553A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
           PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085697
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Desnoyers, Luc
Eaton, Dan
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PRIOR APPLICATION NUMBER: 60/079664
PRIOR FILING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-27
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PRIOR PILING DATE: 1998-03-30
PRIOR APPLICATION NUMBER: 60/080105
PRIOR PILING DATE: 1998-03-31
PRIOR APPLICATION NUMBER: 60/080105
PRIOR PILING DATE: 1998-03-31
PRIOR PILING DATE: 1998-04-01
PRIOR PILING DATE: 1998-04-08
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REPLICATION NUMBER: 60/077791
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REPLICATION NUMBER: 60/077791
REPLICATION NUMBER: 60/07804
REPLICATION NUMBER: 60/07886
REPLICATION NUMBER: 60/07886
REPLICATION NUMBER: 60/078936
REPLICATION NUMBER: 60/078930
REPLICATION NUMBER: 60/078930
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REPLICATION NUMBER: 60/079294
REPLICATION NUMBER: 60/079656
REPLICATION NUMBER: 60/079659
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R APPLICATION NUMBER: 60/077632
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PRIOR FILING DATE: 1998-04-08
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APPLICATION NUMBER: 60/081229
FFLING DATE: 1998-04-09
APPLICATION NUMBER: 60/081955
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FILING DATE: 1997-11-21
APPLICATION NUMBER: 60/077450
FILING DATE: 1997-11-03
APPLICATION NUMBER: 60/065311
FILING DATE: 1997-11-13
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PRIOR FILING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-15
PRIOR APPLICATION WHERE: 60/081819
PRIOR PLING DATE: 1998-04-15
PRIOR PLING DATE: 1998-04-22
PRIOR PLING DATE: 1998-04-29
PRIOR PLING DATE: 1998-05-07
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Best Local Similarity 99.4%; Pred. No. 1.6e-178;
Matches 343; Conservative 2; Mismatches 0;
           PRIOR FILING DATE: 1998-05-15
PRIOR PELING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085700
PRIOR PLING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR PLING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/08550
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PRIOR APPLICATION NUMBER: 60/085573
PRIOR PILING DATE: 1998-05-15
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PRIOR PLING DATE: 1998-05-15
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Grimaldi, J. Christopher
APPLICATION NUMBER: 60/085582
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Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
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Roy, Margaret Ann
Shelton, David L.
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Filvaroff, Ellen
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Gerritsen, Mary E.
Goddard, Audrey
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Eaton, Dan
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Gao, Wei-Qiang
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US-09-999-832A-488
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APPLICATION NUMBER: 66/080333
FILING DATE: 1998-04-01
APPLICATION NUMBER: 66/080334
FILING DATE: 1998-04-01
Stewart, Timothy A.
Tumas, Daniel
Williams, P. Mickey
Wood, William I.
   APPLICANT:
APPLICANT:
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PRIOR APPLICATION NUMBER: 60/081011
PRIOR APPLICATION NUMBER: 60/081011
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-08
PRIOR PLING DATE: 1998-04-09
PRIOR PELICATION NUMBER: 60/081819
PRIOR PELING DATE: 1998-04-15
PRIOR PELING DATE: 1998-04-12
PRIOR PELING DATE: 1998-04-29
PRIOR PELING DATE: 1998-04-R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081049
R FILING DATE: 1998-04-08
R FILING DATE: 1998-04-08
R FILING DATE: 1998-04-08
R APPLICATION NUMBER: 60/081195 APPLICATION NUMBER: 60/081070

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APPLICANT: Par, James;
APPLICANT: Pan, James;
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: William: P. Mickey
APPLICANT: William: P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLC7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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PRIOR PEDILICATION NUMBER: 00/06220
PRIOR FILING DATE: 1997-10-17
PRIOR PEDILICATION NUMBER: 60/062249
PRIOR FILING DATE: 1997-10-17
PRIOR PELING DATE: 1997-10-17
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-03
PRIOR PELING DATE: 1997-11-21
PRIOR PELING DATE: 1998-03-10
PRIOR PELING DATE: 1998-03-11
PRIOR PELING DATE: 1998-03-12
PRIOR PELING DATE: 1998-03-13
PRIOR PELING DATE: 1998-03-13
PRIOR PELING DATE: 1998-03-13
PRIOR PELING DATE: 1998-03-20
PRIOR PELING DATE: 1998-03-27
PRIOR APPLICATION NUMBER: 60/07966
PRIOR APPLICATION NUMBER: 60/07966
PRIOR PELING DATE: 1998-03-27
PRIOR PELING DATE: 1998-03-3-27
PRIOR PELING DATE: 1998-03-3-27
PRIOR PELING DATE: 1998-03-3-3
PRIOR PELING DATE: 1998-
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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                                                  APPLICANT:
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R APPLICATION NUMBER: 60/084600

R APPLICATION NUMBER: 60/084627

R APPLICATION NUMBER: 60/084627

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-07

R FILING DATE: 1998-05-13

R PELING DATE: 1998-05-13

R PELING DATE: 1998-05-13

R PELING DATE: 1998-05-13

R FLING DATE: 1998-05-13

R FLING DATE: 1998-05-13

R PLING DATE: 1998-05-15

R PLING DATE: 1998-05-15
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Publication No. US20030004102A1
GENERAL INFORMATION:
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Oiang
Gerber, Hanspeter
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Baton, Dan
APPLICANT: Baton, Dan
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Best Local Similarity 99.49
Matches 343; Conservative
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1998-03-31 NUMBER: 60/080165 1998-03-31 NUMBER: 60/080194 1998-03-31 1998-04-01 NUMBER: 60/080328 1998-04-01 NUMBER: 60/080333 1998-04-01 1998-04-01 NUMBER: 60/080334 1998-04-01 NUMBER: 60/08034	1998- 1998-	NUMBER: 60/08296 1998-04-23 NUMBER: 60/08336 1998-04-27 NUMBER: 60/08332 1998-04-28 1998-04-29 NUMBER: 60/083495 1998-04-29 NUMBER: 60/083496 1998-04-29 1998-04-29 NUMBER: 60/083495 1998-04-29 NUMBER: 60/083495 1998-04-29 NUMBER: 60/08354 1998-04-29 NUMBER: 60/08358 1998-04-29 NUMBER: 60/08358 NUMBER: 60/08358 1998-04-29 NUMBER: 60/08358 NUMBER: 60/08358 NUMBER: 60/08358 NUMBER: 60/08358 NUMBER: 60/08358 NUMBER: 60/08358 NUMBER: 60/08358
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PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120 61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEFSDGTIL 120 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180 LPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240 LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECOCVPSK 300 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS Gaps 0; Length 345; 301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEEDGCVCRGSTGG 345 Indels Query Match 99.6%; Score 1851; DB 11; Best Local Similarity 99.4%; Pred. No. 1.6e-178; Matches 343; Conservative 2; Mismatches 0; FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085580 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085704 FILING DATE: 1998-05-15 APPLICATION NUMBER: 60/085697 APPLICATION NUMBER: 60/085573 FILING DATE: 1998-05-15 61 181 241 121 PRIOR
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RESULT 14 US-09-796-753-6

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1 MSLFGLLLLTSALAGQRQGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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                                                                         HENERAL INFORMATION:
APPLICANT: MCGATCHY, Sean A.
APPLICANT: MCGATCHY, SECRETED PROTEINS AND USES THEREOF FILE OF INVENTION: SECRETED PROTEINS AND USES THEREOF FILE REFERENCE: 7853-227-999
CURRENT APPLICATION NUMBER: US/09/796,753
CURRENT FILING DATE: 2091-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-10-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
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PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR FILING DATE: 1998-12-30
PRIOR PLILING DATE: 1998-12-30
PRIOR PLILING DATE: 1999-02-26
PRIOR PLILING DATE: 1999-03-01
PRIOR PLILING DATE: 1999-03-01
PRIOR PLILING DATE: 1999-03-01
PRIOR PLILING DATE: 1999-06-18
PRIOR PLILING DATE: 1999-06-29
PRIOR PLILING DATE: 1999-09-20
PRIOR PLILING DATE: 1999-12-29
PRIOR PLILING DATE: 2000-02-25
PRIOR PLILING DATE: 2000-03-01
PRIOR PLILING DATE: 2000-06-19
PRIOR PLILING DATE: 2000-06-29
PRIOR PLILING DATE: 2000-06-
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          Sequence 6, Application US/09796753
Publication No. US20030027998A1
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-09-30
NUMBER OF SEQ ID NOS: 162
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Best Local Similarity 99.4%
Matches 343; Conservative
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61 PREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120
                                               61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEBEBSDGTIL 120
                                                                                                  121 GRWCGSGTVPGKQISKGNQIRIRFVSDRYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180
                                                                                                                            181 LPLDLLANNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240
                                                                                                                                                                                                                                    241 LIEEVRLYSCIPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                                                      241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic TITLE OF INVENTION: Acids Encoding the Same FILE REFERENCE: P2630P1C22
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT FILING DATE: 2001-10-16
NUMBER OF SEQ ID NOS: 624
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                                                                                                                                                                                                                                                                                                                                                                                                         301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
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LENGTH: 345
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Grimaldi, J. Christopher
Gurney, Austin L.
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Shelton, David L.
Stewart, Timothy A.
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Filvaroff, Ellen
Fong, Sherman
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Gerritsen, Mary E.
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Kljavin, Ivar J.
Kuo, Sophia S.
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Desnoyers, Luc
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Best Local Similarity 99.4'
Matches 343; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wei-Qiang
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APPLICANT: Baker Kevin P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Homo sapiens
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	61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGTIL 120	61 PRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVERPEDGTIL 120	121 GRWCGSGTVPGKQISKGNQIRIREVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180	121 GRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVSPSVLPPSA 180	181 LPLDLLINNAITARSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKARVFGRKSRVVDLNL 240	181 LPLDLINNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL 240	241 LTBEVRLYSCTPRNFSVSIRBELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECOCVPSK 300	241 LTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300	301 VTKKYHEVLOLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345	1 VIKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEBCDCVCRGSTGG 345	
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Search completed: November 25, 2003, 21:17:04 Job time: 25.3006 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:59:34; Search time 14.7173 Seconds (without alignments) 2254.373 Million cell updates/sec

Title: US-09-852-209A-3
Perfect score: 1858
Sequence: 1 MSLFGLLLVTSALAGQRRGT.....DVALEHHEECDCVCRGSTGG 345

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5 Total number of hits satisfying chosen parameters: 283308

283308 seqs, 96168682 residues

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : PIR_76:*
1: Dir1:*
2: Dir2:*
3: Dir3:*
4: Dir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

335 CDCVC 339

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TSG-6 homolog PS4	16K vascular endot	platelet-derived g	platelet-derived g	platelet-derived g	platelet-derived g	UVS.2 protein - Af	sanko - human	platelet-derived g	platelet-derived g	PDGF-related trans	platelet-derived g	vascular endotheli	platelet-derived g	platelet-derived g	protein F57C12.1 [
A47290	D49530	PFHUG2	151551	508220	IS1550	151569	A59386	JN0248	\$25096	TVMVSS	A37359	A41551	B28964	PFHUG1	D89447
~	η.	-	N	N	~	N	~	8	7	Н	N	0	N	П	N
276 2	148 2	241 1	200 2	215 2	226 2	319 2	2403 2	166 2	197 2	226 1	196 2	232 2	196 2	211 1	770 2
6.4 276 2															
	6.2	6.2	6.1	6.1	6.1	6.0	5.9	υ. 6.	5.9	5.8	8.8	5.6	5.6		5,5

ALIGNMENTS

RESULT 1 UG7591 UG7591 Species 190-Unu-2001 C.Accesion: JG7591 Richamada, T.; U1-2001 Richamada, T.; U1-2001 Richamada, T.; U1-Rei A.File Molecular C A.Feference number: A.Feferences: 1-370 cH A.Fesidues: 1-370 cH A.Fesidues: 1-370 cH A.Fesidues: 1-370 cH A.Ferences: 1-370 cH A.Forosa references: 1-370 cH B.Forosa references: 1-3	RESULT 1 spinal cord-derived growth factor-B precursor - human c;Speciae; Homo sapiens (man) C;Accession: JC7591 C;Accession: JC7591 C;Accession: JC7591 C;Accession: JC7591 A;Itle: Molecular cloning of SCDGF-B, a novel growth factor homologous to SCDGF/PDGP-A;Retearce number: JC7591; MUID:21092670; PMID:1116282 A;Residues: 1-370 A;Residues: 1-370 A;Accession: JC7591 A;Accession: JC7501 A;Accession: JC7501 A;Acces	cch larity 43.6%; Score 742.5; DB 2; Length 370; al Similarity 43.6%; Pred. No. 9e-57; 159; Conservative 59; Mismatches 114; Indels 33; Gaps 10;	LFGLLLVTSALAGGRRGTQAESNLSSKRQFSSNKEQNGVOD-PQHERIITVSTNGSI	5 IFVYTLICANFCSCRDTSATPQSASIKALRNANLRRDESNHLTDLYRRDETIQVKGNGYV 64	59 HSPRFPHTYPRNTVLVWRLVAVERNVMIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT 118	9ILGRWCGSGTVPGKQISKGNQIRIRRVSDEYFPSEPGFCIHYNIVMPQFTEAV 171 	3 WESVTSSISGVSYNSPSVTDPT-LIADALDKKIARPDTVEDLIKYFNPBSWQEDLENMYL 241	8 PIWQLIGKAFVFGRKSRVVDLNLITEEVRLYSCTPRNFSVSIREELKRTDTIFWFGCLLV 277	DTPRYRGRSY-HSRKSK-VDLDRLNDDAKRYSCTPRNYS	278 KRCGGNCACCLHNCNECQCVPSKVTKKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEE 334	O ORČGGNČGČGTVNMRSČTČNSGKTVKKYHEVLOFRÞGHIKRRGRAKTMALVÞÍOLDHHER 359
	ESULT 1 (7591 Pinal cord-); Species: H); Accession: (1,04mm about 1,04mm about 1,	Query Matc Best Local Matches 1	<u>ک</u>	ą							

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A; pescription: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty Sisuperfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; Clr/Cls repeat homology; Clr/Cls repeat homology; Clr/Cls repeat homology; Fi.2-27 bomain: signal sequence #stauts predicted <arg. calcium; duplication; Fi.3-27 bomain: signal sequence #stauts predicted calcs.
Fi.3-27 bomain: stacin homology <asg. calcium; MPPI #status predicted <MAT>Fi.32-431/bomain: astacin homology <asg. calcium; Clr/Cls repeat homology <clr>Fi.35-1-587/bomain: Clr/Cls repeat homology <clr>Fi.551-587/bomain: Clr/Cls repeat homology <clr>Fi.551-587/bomain: Clr/Cls repeat homology <clr>Fi.51-700/bomain: Clr/Cls repeat homology <clr>Fi.51-100/bomain: Clr/Cls repeat homology <clr>Fi.100-100/bomain: Clr/Cls repeat homology <clr>Fi.100-100/bomain: Clr/Cls repeat homology <clr>Fi.51-100/bomain: Clr/Cls repeat homology <clr>Fi.51-100/bomain: Clr/Cls repeat homology <clr>Fi.51-100/bomain: Clr/Cls repeat homology <clr>Fi.51-100/bomain: Clr/Cls repeat homology <clr>Fi.100-100/bomain: Clr/Cls repeat homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1159 DGS--STGCGCN----LTTSSGTFISPNYPMPYYHSSECYWWLKSSHG-SAFELEFKDFH 1211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 SGTVPGKQISKGNQIRIRFVSDEYFPSBPGFCIHYNIV-----MPQFTEAVSPSVLPPS 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            272 PGCLLVKRCGGNCACCLHNCNECOCVPSKVTKKYHE----VLQLRPKTGVRGLHKSLTDVA 328
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           - human
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C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Saccession: A37278; Es6788
R.Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kriz Science 242, 1528-1534, 1988
A.Title: Novel regulators of bone formation: molecular clones and activities. A.Reference number: A37278; MUID:88072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              951 VYPHGINCTWHIL-VQPNHLIHLMF-ETFHLEFHYN--CTNDYLEVYDTDSETSLGRYCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           66 TYPRNTVLVWRLVAVBENVWIQLTFDERFGLEDPEDDICKYDFVEVEPSDGTILGRWCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ::| : | | | : : | | : | | : | | : | | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  19 GTQAESNLSSKFQF----SSNKEQNG-----VQDPQHERIITVSTNGSIHSPRFPH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           180 ALPLDLLUNAITAFSTLEDLIRYLEPERWOLDLEDLYR---PTWOLLGKAFVFGRKSRVV
                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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A; Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
                                                                                                                                                                             <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                 90;
C,Superfamily: intrinsic factor-Bl2 receptor cubilin; EGF homology C;Keywords: receptor; vitamin Bl2 uptake F;1-24/Domain: signal sequence #status predicted <SIG> F;1-24/Domain: signal sequence #status predicted <SIG> F;25-3623/Product: intrinsic factor-Bl2 receptor #status predicted F;436-467/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                               Length 3623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         237 DINLLTE--EVR-------LY--SCTPRNFSVSIREELK-RTDTI-
                                                                                                                                                                                                                                                                                                               9.8%; Score 183; DB 2; Length 36;
6.2%; Pred. No. 8.2e-07;
ve 42; Mismatches 139; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GDB:125203; OMIM:112264
A; Map position: 8p21-8p21
C; Function:
                                                                                                                                                                                                                                                                                                                                                                          26.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                           96; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                Similarity
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Best Local S:
Matches 96,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1-17/Domain: secretory signal sequence #status predicted <SIG>
18-370/Product: spinal cord-derived growth factor-B #status predicted <MAT>
52-170/Region: CUB domain #status predicted
;272-370/Region: homologous to platele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to SCDGF/PDGF-C/
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C;Species: Homo sapiens (man)
C;Date: 16-U1-1999 #sequence_revision 16-Jul-1999 #text_change 02-Aug-2002
C;Accession: T109456
R;Kozyraki, R.; Kristiansen, M.; Silahtaroglu, A.; Hansen, C.; Jacobsen, C.; Tommerup,
Blood 91, 3593-3600, 1998
A;Title: The human intrinsic factor-vitamin B12 receptor, cubilin: Molecular character:
                                                                                                                                                                                                                                        Cipate: 30-July cord-derived growth factor-B precursor - rat
Cipate: Satus norvegicus (Norway rat)
Cipate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #text_change 24-Aug-2001
Cipate: 30-Jun-2001 #sequence_revision 30-Jun-2001 #sequence procession: Aignorial ration of SCOGFP, A. novel growth factor homologous to SCOGFP
Aignorial ration and Daylor SCOGFP, A. Nolecule type: mRNA
Aignorial ration and Aignorial Residues and Aignorial ration and Aignorial
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A)Accession: 109456
A)Status: preliminary; translated from GB/EMBL/DDBJ
A)MOLecule type: mRNA
A)Rosion: 1-3623 «ROZ»
A)Cross-references: EMBL:AF034611; NID:g3929528; PIDN:AAC82612.1; PID:g3929529
C)Genetics:
A)Map position: 10p12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE 153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNF 255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.6%; Score 736; DB 2; Best Local Similarity 45.6%; Pred. No. 3.3e-56; Matches 149; Conservative 57; Mismatches 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -KTGVRGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FXRRGKAKNMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PGFCIHYNIV---MPQFTEAV----
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C.Superfamily: intrinsic factor-B12 receptor cubilin, EGF homology
C;Keywords: egg yolk; endocytosis; glycoprotein; intestine; kidney; peripheral membran:
F;1-20/Domain: signal sequence #status predicted <SIG>
F;1-23/Product: intrinsic factor-B12 receptor CUBILIN #status predicted <MAT>
F;13-164/Domain: EGF homology <EGF1>
F;436-467/Domain: EGF homology <EGF>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Moestrup, S.K.; Kozyraki, R.; Kristiansen, M.; Kaysen, J.H.; Rasmussen, H.H.; Brault J. Bis. 273, 5235-5242, 1998
A;Title: The intrinsic factor-vitamin Bl2 receptor and target of teratogenic antibodies A;Reference number: 216459; MUID:98148073; PMID:9478979
                 A;Title: Cloning and expression of cDNA encoding Xenopus laevis bone morphogenetic prol
A;Reference number: JC2218; MUID:94085787; PMID:8262384
A;Accession: JC2218
                                                                                                                                                                                                                                                                             C; Comment: This protein induces ectopic cartilage formation in vivo.
C; Comment: This protein induces ectopic cartilage formation in vivo.
C; Superfamily: procollagen C-endopeptidase; astacin homology; Clr/Cls repeat homology; Clr/Cls repeat homology; AST>
F; 93-284/Domain: astacin homology cAST>
F; 85-397/Region: complement lr/Is-like repeat
F; 285-394/Domain: Clr/Cls repeat homology cClRl>
F; 388-507/Domain: Clr/Cls repeat homology cClRl>
F; 388-507/Domain: Glr/Cls repeat homology cClRl>
F; 514-550/Domain: Glr/Cls repeat homology cClRl>
F; 514-550/Domain: Glr/Cls repeat homology cClRl>
F; 554-666(Region: complement lr/Is-like repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         945 SPGHPNVYPRGVNCTWHVV-VQRGQLIRLEFSS-FYLEFHYN--CTNDYLEIYDTAAQTF 1000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      55 NGSIHSPRFFHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL;AF022247; NID;g3834379; PIDN:AAC71661.1; PID:g3834380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 SPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEVEEPSDGTI 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               120 LGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY-----NIVMPQFTEAVSP 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 SLFGLLLVT--SALAGQRRGTQAESNLSSKFQFSSNKBQNGVQDPQHERIITVSTNGSIH 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C:Species: Rattus norvegicus (Norway rât)
C:Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 02-Aug-2002
C;Accession: T08618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F;554-663/Domain: CIr/CIS repeat homology <CIR3>
F;62,105,295,326/Binding site: carbohydrate (Asn) (covalent) #status predict
F:175,180,186,235/Binding site: zinc (His, His, His, Tyr) #status predicted
F:177/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;528/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 92; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Gaps
                                                                                                                                                                      A;Molecule type: mRNA
A;Residues: 1-707 <MAE>
A;Cross-references: GB:L12249; NID:9406540; PIDN:AAA16313.1; PID:9406541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9.5%; Score 176; DB 2; Length 3623; 25.5%; Pred, No. 3.3e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114 -PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  618 LTSDSKLHGKFCGS-ELPAVITSQYNNMRIEFKSDNTV-SKKGF 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15; Mismatches 36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25.5%; Pred. No. 3.3e-vo; tive 52; Mismatches 133; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                intrinsic factor-B12 receptor CUBILIN precursor - rat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      / Match 9.5%; Score 176; DB 2; Local Similarity 43.3%; Pred. No. 4.2e-07; nes 45; Conservative 15; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 25.59
Matches 95; Conservative
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Gene 134, 257-261, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 5
JOOGA8
A5 antigen precursor - African clawed frog
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: Xenopus laevis (African clawed frog)
C; Species: Sep-1999 #sequence_revision 10-Sep-1999 #text_change 16-Jun-2000
C; Accession: JH0466; JOOG48
R; Takagi, S.; Hirata, T.; Agata, K.; Mochii, M.; Eguchi, G.; Fujisawa, H.
Neuron 7, 295-307, 1991
A; Title: The A5 antigen, a candidate for the neuronal recognition molecule, has homologi
A; Reference number: JH0466; MUID:91337458; PMID:1908252
A; Residues: 1-927 - TAKA
A; Res
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        F,150,261,300,523,844/Binding site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                               7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMP-- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       88 EVIDGDNANGQLLGKYCGK-IAPSPLVSTGPSIFIRFVSDYETPG-AGFSIRYEVFKTGP 145
                                                                                                                                                                                                                                                       55 NGSIHSPREPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKXDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                        599 NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFETEG-----NDVCKYDFVEVRS 653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              114 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAV 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 IKITSPSYLTSAGYPHSYPPSQRCEWLIQAPEHYQRIMINFNPHFDLEDRE---CKYDYV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  procollagen C-endopeptidase (EC 3.4.24.19) - African clawed frog (clone 22AN) N;Alternate names: bone morphogenic protein 1 C;Species: Xenopus laevis (African clawed frog) C;Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 20-Sep-1999 C;Accession: JC2218 K;Maeno, M.; Xue, Y.; Wood, T.I.; Ong, R.C.; Kung, H.
        F;565/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                          17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            166 ----QFTEA--VSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 927;
                                                                            ch 1 Similarity 37.3%; Score 181.5; DB 1; Length 730; Similarity 37.3%; Pred. No. 1.4e-07; 50; Conservative 20; Mismatches 47; Indels 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         9.7%; Score 179.5; DB 1; Length 9
31.6%; Pred. No. 2.9e-07;
tive 29; Mismatches 73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 SPSVLPPSALPLDL 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         705 RPALQPPRGRPHQL 718
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 31.6
Matches 55, Conservative
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                                                                                                  Query Match
Best Local
                                                                                                                                                                          Matches
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A; Description: catalyzes hydrolysis of the carboxyl-terminal propeptide of collagen ty C; Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cis repeat homology; C; Superfamily: procollagen C-endopeptidase; astacin homology; Cir/Cis repeat homology; C; Keywords: alternative splicing; beta-hydroxyasparagine; bone; calcium; duplication; F; 12-22/Domain: signal sequence #status predicted <SIG>
F; 23-986/Product: procollagen C-endopeptidase tolloid-like splice form #status predict; F; 130-321/Domain: cir/Cis repeat homology <AST>
F; 130-321/Domain: Cir/Cis repeat homology <CiR2>
F; 551-587/Domain: Cir/Cis repeat homology <CiR2>
F; 551-587/Domain: Cir/Cis repeat homology <CiR3>
F; 551-700/Domain: Cir/Cis repeat homology <CiR3>
F; 707-742/Domain: Cir/Cis repeat homology <CiR4>
F; 747-856/Domain: Cir/Cis repeat homology <CiR4>
F; 760-973/Domain: Cir/Cis repeat homology <CiR4>
F; 760-973/Domain: Cir/Cis repeat homology <CiR5>
F; 770-742/Domain: Cir/Cis repeat homology <CiR5>

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F/91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/91,142,332,363,599/Binding site: carbohydrate (Asn) (covalent) #status predicted
F/163-217,223,272/Binding site: zinc (His, His, His, Tyr) #status predicted
F/214/Active site: Glu #status predicted
F/565,720/Modified site: erythro-beta-hydroxyasparagine (Asn) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                    - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice form - mouse C;Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Residues: 1-702, EKRPALQPPRGRPHQLKFRVQKRNRTPQ' <WOZ>
A; Cross-references: GB:M22488; NID:g179499; PIDN:AAA51833.1; PID:g179500
R; Takahara, K.; Lyons, G.E.; Greenspan, D.S.
B; Takahara, K.; Lyons, G.E.; Greenspan, D.S.
A; Title: Bone morphogenetic protein-1 and a mammalian tolloid homologue (mTld) are A; Reference number: A58788; MUID:95096114; PMID:7798260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                        splice form
        --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDBYFPSEPGFCIHYNIVMPQFTEAV 171
                                                                            654 GLIADSKIHGKFCGS-EKPEVITSOYNNMRVEFKSDNTV-SKKGFKAHFFSVLEGAGDRH 711
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M.J.; Kriz,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEBNVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              activities
                                                                                                                                                                                                                                                                                                                                                                                                                           procollagen C-endopeptidase (EC 3.4.24.19) precursor, tolloid-like splice for N;Alternate names: bone morphogenic protein 1, tolloid-like splice form C;Species: Homo sapiens (man)
C;Date: 28-Mar.1998 #sequence_revision 09-Apr.1998 #text_change 16-Jul-1999 C;Accession: A37278; BS8788
R;Wozney, J.M.; Rosen, V.; Celeste, A.J.; Mitsock, L.M.; Whitters, M.J.; Kri Science 242, 1528-1534, 1988
A;Title: Novel regulators of bone formation: molecular clones and activities A;Reference number: A37278; MUID:89072730; PMID:3201241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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A;Residues: 703-986 <TAK>
A;Cross-references: GB:L35279; NID:g619860; PIDN:AAC41710.1; PID:g619861
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; Score 169; DB 1; Length 986;
; Pred. No. 2.6e-06;
17; Mismatches 39; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SHLSGLELLLCPHALVDTVPAPPSAL 737
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A,Gene: GDB:BMP1; BMP-1
A,Cross-references: GDB:125203; OMIM:112264
A,Map position: 8p21-8p21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Accession: A37278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Accession: B58788
                                                                                                                                                             172
                                                                                                                                                                                                                                      712
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RESOLT
---YWDGS--STGCGGN----LTTPTGVLTSPNYPMPYYHSSECYWRLEASHG-SPFELE 1206
                                                                                                                                                                                                                                                                          DLYRPTWQLLGKAFVFGRKSRVVDLNLLTEEVRLY-----SCTPRNFSVSIREELKRT 266
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                                                                                                                                                                                                                                                                                                                                                                                                                                    267 DIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHE---VLQLRPKTGVRGLHKS 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             653
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                                                                                                                                                                                                                                                                                                                                                   1111 DGGYETSPLVG---IY---CGSVLPPTIISHSNKLWLKFKSDAALTAKGFSA-
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35.6%; Pred. No. 9.2e-07;
iive 19; Mismatches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1207 FODFHLEHHPSC 1218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     324 LTDVALEHHEEC 335
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                                                                                                                     SVLP--PSALPLDL
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C,Accession: A59271
R;Thiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, S.Nthiel, S.; Vorup-Jensen, T.; Stover, C.M.; Schwaeble, W.J.; Laursen, S.B.; Poulsen, Nature 386, 506-510, 1997
A;Title: A second serine protease associated with mannan-binding lectin that activates A;Reference number: A59271; MUID:97242412; PMID:9087411
                                                                                                                                                                                                                                                                                                                                                                                            "Coral-ventral patterning protein tolloid (EC 3.4.24.-) - fruit fly (Drosophila melano C; Species: Drosophila melanogaster C; Species: 10-Sep-1999 #text_change 10-Sep-1999 C; Accession: A39288 R; Shimell M.J.; Ferguson, E.L.; Childs, S.R.; O'Connor, M.B. Cell F7, 469-481, 1991 A; Title: The Drosophila dorsal-ventral patterning gene tolloid is related to human bon A; Reference number: A39288; MUID:92034970; PMID:1840509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cones references: FlyBase: FBgn0003719
C; Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls re C; Superfamily: dorsal-ventral patterning protein tolloid; astacin homology; Clr/Cls references: duplication; hydrolase; metalloproteinase; zinc
C; Keywords: duplication; hydrolase; metalloproteinase; zinc
F; 329-464/Domain: castacin homology <AST>
F; 352-464/Domain: Clr/Cls repeat homology <ClR2>
F; 585-620/Domain: EGF homology <EG1>
F; 585-620/Domain: EGF homology <EG2>
F; 747-782/Domain: Clr/Cls repeat homology <ClR3>
F; 747-782/Domain: Clr/Cls repeat homology <ClR3>
F; 787-896/Domain: Clr/Cls repeat homology <ClR5>
F; 781, 285, 231, 280/Binding site: zinc (His, His, His, Tyr) #status predicted
F; 222/Active site: Glu #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         parts of this sequence, including the amino end of the mature protein, were del
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N/Alternate names: mannose binding protein-associated serine proteinase 2 (MASP-2)
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224 AVSDDSRRLGKFCGD-AVPGSISSECNELLVQFVSDLSVTAD-GFSASYK-TLPRGTAKE 280
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C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 16-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A;Residues: 1-686 <JEN>
A;Residues: 1-686 <JEN>
A;Across-references: GRY09926; NID:g4007626; PIDN:CAA71059.1; PID:g4007627
A;Experimental source: tissue liver
A;Note: submitted to GenBank, December 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Cross-references: GB:M76976; NID:g157305; PIDN:AAA28491.1; PID:g157306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 1057;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.0%; Score 148.5; DB 1;
18.0%; Pred. No. 0.00017;
                                                                                                 169 -----EAVSPSV-LPPSALP 182
                                                                                                                                                                                    281 GOGPGPKRGTEPKVKLPPKSOP 302
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 38.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-1057 <SHI>
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                                       C. Jates 102-011-1930 #Sequence_revision 02-011-1930 #CACCESSION: 149540

R. Fukagawa, M.; Noboru, S.; Hogan, B.L.M.; Jones, C.M.

Dev. Biol.: 163, 175-183, 1994

A; Title: Embryonic expression of mouse bone morphogenetic protein-1 (BMP-1) which is rell
A; Reference number: 149540; MUID:94229342; PMID:817472

A; Reference number: 149540; MUID:94229342; PMID:817472

A; Reference number: 149540; MUID:94229342; PMID:817472

A; Reference number: 149540; MUID:9429342; PMID:817472

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A; Reterence number: 149540; MUID:9429342; PMID:817472

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Aigenetics:
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Cisuperfamily: C1r/C1s repeat homology
Cisuperfamily: C1r/C1s repeat homology
Cisuperfamily: C1r/C1s repeat homology
Cisuperfamily: C1r/C1s repeat homology c1R1>
Fig.449/Product: #status predicted <MAT>
Fig.446/Domain: C1r/C1s repeat homology <C1R1>
Fig.546/Domain: C1r/C1s repeat homology c1R1>
Fig.6/Modified site: pyrrolidone carboxylic acid (Gln) (in mature form) #status predicted F;26/Modified site: carbohydrate (Asn) (covalent) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Takahara, K.; Kessler, E.; Biniaminov, L.; Brusel, M.; Eddy, R.L.; Jani-Sait, S.; Show J. Biol. Chem. 269, 26280-26285, 1994
A;Title: Type I procollagen COOH-terminal proteinase enhancer protein: identification, p. A;Reference number: A55362; MUID:95014462; PMID:7523404
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       112 EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFT--- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     604 NGSITSPGWPKEYPPNKNCIWQLVAPTQYRISLQFDFFFTEG-----NDVCKYDFVEVRS 658
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C;Species: Homo sapiens (man)
C;Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C;Accession: A5536
B;Takahara, K.; Kessler, E.; Biniaminov, I.; Brusel, M.: Eddv p 7 .....
         C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jan-2000
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9.1%; Score 169; DB 2; Length 991;
Best Local Similarity 39.4%; Pred. No. 2.6e-06;
Matches 43; Conservative 17; Mismatches 39; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels 22; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       659 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705
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A; Residues: 1-449 <TAK>
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A; Accession: A55362
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A;Cross-references: GDB:6071500

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Search completed: November 25, 2003, 21:05:29 Job time: 15.7173 secs
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tolloid-BMP-1 like protein 1 - California sea hare
tolloid-BMP-1 like protein 1 - California sea hare
tolloid-BMP-1 like protein 1 - California sea hare
tolloid-BMP-1 like protein 1 - California sea hare)
C;Species: Aplysia californica (California sea hare)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 18-Aug-2000
C;Accession: T31069
Taltar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es
T;Liu, O.R.; Hattar, S.; Endo, S.; MacPhee, K.; Zhang, H.; Cleary, L.J.; Byrne, J.H.; Es
A;Title: A developmental gene (Tolloid/BMP-1) is regulated in Aplysia Neurons by treatme
A;Reference number: 220965; MUID:98007484; PMID:8987797
A;Reterence number: Translated from GB/EMBL/DDBJ
A;Accession: T31069
A;Accession: T31069
A;Residues: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1070 <LLU>
C;Superfemences: EMBL:U57369; NID:91899041; PID:91899042; PIDN:AAC47485.1
C;Superfemmily: dorsal-ventral patterning protein tolloid; astacin homology; CIr/CIs repe
A;Map position: 1p36.2-lp36.3
C;Superfamily: complement subcomponent Clr; Clr/Cls repeat homology; complement factor H
C;Superfamily: complement subcomponent pathway; duplication; hydrolase, serine F
F;1-15/Domain: signal sequence #status predicted <SIG>
F;1-15/Domain: signal sequence #status predicted <SIG>
F;16-44,445-686/Product: Ra-reactive factor 2 #status predicted <MAT>
F;19-134/Domain: Clr/Cls repeat homology <CIR1>
F;142-180/Domain: BGF homology <EGF>
F;142-180/Domain: Clr/Cls repeat homology <CIR2>
F;346-233/Domain: complement factor H repeat homology <FH1>
F;366-430/Domain: complement factor H repeat homology <FH2>
F;366-430/Domain: cymplement factor H repeat homology <FH2>
F;445-679/Domain: cymplement factor H repeat homology <FH2>
F;446-679/Domain: cymplement factor H repeat homology <FH2>
F;446-679/Domain: cymplement factor H repeat homology <FH2>
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F;447-445-679/Domain: cymplement factor H repeat homology <FH2>
F;448-445-679/Domain: cymplement factor H repeat homology <FH2>
F;448-445-679/Domain: cy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | ::|| :| | :| | :| | :| | GFLNSPAYDEYGSDKVCEW-VITVREGYQVALEFATFETEF---DPD---CAYDYVEIR 581
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        176 LPPSALPLDLLNNAITARS----TLEDLIRYLEPERWQLDLEDLYRPTWQLLGKARVFG 230
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ----NIVMPOFTEAUSPSV 175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       231 RKSRVVDLNLLTEEVRLYSCTPRNFSVS--IREELKRTDTIFWPGCLL-----VKRCGGN 283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    742 NKER-----LOGOYCGFWAPPSITSLSNELRIBFRSDDTLOKTGFSMDYVADVDECASS 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               115 SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 7.5%; Score 139.5; DB 2; Local Similarity 21.9%; Pred. No. 0.0011; es 70; Conservative 36; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.7%; Score 143.5; DB 1
32.1%; Pred. No. 0.00027;
tive 25; Mismatches 42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 284 CACCLHNCN-----ECQC 296
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 7.7
Best Local Similarity 32.1
Matches 34; Conservative
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Best Local S
Matches 70
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A, Status: preliminary
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Molecule type: mRNA
A, Residues: 1-7, 8', 9-10, V', 12-28, 'H', 30-72,'D', 74-77,'SK', 80-81,'I', 83-232,'R', 234-2
9-571,'N', 573-58,'D', 586-595,'D', 597 < LEP>
A, Cross-references: EMBL:X56224; NID:g10928; PID:g10929
A, Experimental source: embryo
A, Experimental source extracted from NCBI backbone (NCBIP:99979)
         - sea urchin (Paracentrotus liv
                                                                                                                                                                                                                                                                                                     metalloproteinase (EC 3.4.24.-) 10 precursor, blastula - sea urchin (Paracentrotus liv N;Alernate names: gene tolloid protein homolog C;Species: Paracentrotus lividus (common urchin) C;Date: 12-Feb-1998 #sequence revision 13-Mar-1998 #text_change 17-Mar-1999 C;Accession: S71352; A44880; S22060 Ex;Lhomond, G.; Ghigilione, C.; Lepage, T.; Gache, C. Bur. J. Biochem. 238, 744-751, 1996 A;Title: Structure of the gene encoding the sea urchin blastula protease 10 (BP10), a M;Reference number: S71352; MUID:96300240; PMID:8706676
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GVITSPNWPGRYDDNMACVYQIEGPPGST-IELTFTE---MNIENHAVCRYDAVEIRKDD 403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 --SDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFTEAVS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         459 TITI-SITIPVPTITQATIDETVVGSCGGRFGGIQGRVATPNY--PNNYDNDL/CVYVIE 515
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            173 PSVLPPSALPLDLLNNAIT------AFSTLEDLI---RYLEPERWQLDLEDLYRPT 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        220 WQLLGKAFVFGRKSRVVDLNLLTEEVRLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKR 279
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ---IDMKM 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVERP-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Introns: 30/3; 116/1; 184/3; 252/3; 370/3; 555/2
C;Superfamily: Clr/Cls repeat homology; astacin homology
C;Keywords: hydrolase; metalloproteinase; zinc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7.5%; Score 138.5; DB 2; 24.4%; Pred. No. 0.00062;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 24.4%
Matches 59; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: November 25, 2003, 20:55:48; Search time 8.55655 Seconds (without alignments) 1896.117 Million cell updates/sec

US-09-852-209A-3

Perfect score: 1858 Sequence: 1 MSLFGLLIVTSALAGQRRGT......DVALEHHEECDCVCRGSTGG 345

Searched: 127863 segs, 47026705 residues

Gapop 10.0 , Gapext 0.5

BLOSUM62

Scoring table:

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

SUMMARIES	ID Description	1 NRP1 XENLA P28824 xenopus lae	0 xenopus	STRPU P98068 strongyl	~	1 BMP1 MOUSE P98063 mus musculu	HUMAN	RAT 09qwj9	RAT			E 035375 1	1 TLD_BRARE O57460 brachydanio	و	P79795	015113	P25723	043915	000187	P97946 mus m		P98064		1 CIR HUMAN P00736 homo sapien	P48740		SE Q61398	008628	RABIT	P97953	HUMAN P98066	1 PDGB_FELCA P12919 felis silve	
	Length DB	928	707	616	986	166	931	922	925	326	923	931	1022	923	914	449	1057	354	989	358	597	704	639	705	669	419	468	468	213	415	277	245	
•	CT (B)	9.7	9.5	9.3	9.1	9.1	8.9					•		8.5	٠	•	•	7	۲.		۲.	۲.		7.4	•	7.1				6.7	9.9	6.5	
	COL	179.5	176	173.5	169	169	164.5	163.5	163	162.5		•	LO	158.5	157	154	148.5	147	143.5	140	139.5	138.5	138	13	٠	132	2	N	125	N	123.5	120.5	
	ω 🗀		7	М	4	Ŋ	9	7	æ	a	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29	30	31	ć

P52585 orf virus (P01127 homo sapien	P13698 xenopus lae P42664 xenopus lae	P20033 mus musculu P28576 rattus norv	P26617 cavia porce P01128 simian sarc	P49765 homo sapien P15692 homo sapien	P04085 homo sapien P52584 orf virus (
VEGH_ORFN7 PDGB_HUMAN	PDGA_XENLA UVS2_XENLA	PDGA RAT	VEGA_CAVPO TSIS_SMSAV	VEGB HUMAN VEGA HUMAN	PDGA_HUMAN VEGH_ORFN2
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148	514	204	164 226	207	211
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114.5	112.5	109	108.5	105.5	104 102.5
3.4 4.0	34	B 60 9	40 41	43	4 4 5

ALIGNMENTS

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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its web yn non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                              01-DEC-1992 (Rel. 24, Created)
1-DEC-1992 (Rel. 24, Last sequence update)
28-FBB-2003 (Rel. 41, Last amnotation update)
Neuropilin-1 precursor (A5 protein) (A5 antigen).
Renopus laevis (African clawed frog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                                                                                                                                                                 -! - SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             -1- SIMILARITY: Contains 2 CUB domains.
-1- SIMILARITY: Contains 2 F5/8 type C domains.
-1- SIMILARITY: Contains 1 MAM domain.
                          928 AA.
                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000859; CUB domain.
InterPro; IPR000859; CUB domain.
InterPro; IPR000821; FA58 C.
InterPro; IPR000899; MAM domain.
Ffam; PP00431; CUB; 2.
Ffam; PP00629; MAM, 1.
FRINTS; PR00020; MAMDOMAIN.
SWART; SM00442; CUB; 2.
SWART; SM00442; CUB; 2.
SWART; SM00131; FA58C; 2.
SWART; SM00131; RA58C; 2.
FROSITE; PS01180; CUB; 2.
                                                                                                                                                                                                          TISSUE=Brain;
MEDLINE=91337458; PubMed=1908252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; D10467; BAA01260.1; -. HSSP; P12259; 1CZT.
                           STANDARD;
                                                                                                                                                     Xenopodinae; Xenopus.
                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                  NCBI_TaxID=8355;
                           XENLA
RESULT 1
NRP1_XENLA
                             NRP1
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88 EVIDGDNANGQLLGKYCGK-IAPSPLVSTGPSIFIRFVSDYETPG-AGFSIRYEVFKTGP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                          50 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMP-- 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  166 ----OFTEA--VSPSVLPPSALPLDLINNAITAFSTLEDLIRYLEPERWQLDLE 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   146 ECSRNFTSSNGVIKSPKYPEKYPNALECTYIIFAPKOQEIV--LEFESFELEAD 197
                                                                Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Maeno M., Xue Y., Wood T.I., Ong R.C., Kung H.F.;
"Cloning and expression of cDNA encoding Xenopus laevis bone
morphogenetic protein-1 during early embryonic development.";
Gene 134:257-261(1993).
-!- FUNCTION: INVOLVED IN PATTERN FORMATION IN GASTRULA AND LATER
DIFFERENTIATION OF DEVELOPING ORGANS.
-!- DEVELOPMENTAL STAGE: BLASTULA, SARLY GASTRULA AND HATCHED
TADPOLES; LITTLE OR NO EXPRESSION IN WORULA AND LATE GASTRULA.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
20-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.-) (BMP-1).
Renoups laevis (African clawed frog).
Eukaryota; Metazoa; Choordata; Craniata; Vertebrata; Buteleostomi; Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                                                                                                                                                                                                                                                                             129 BY SIMILARITY.
150 N-LINKED (GLCNAC. .) (POTENTIAL).
151 N-LINKED (GLCNAC. .) (POTENTIAL).
152 N-LINKED (GLCNAC. .) (POTENTIAL).
153 N-LINKED (GLCNAC. .) (POTENTIAL).
1644 N-LINKED (GLCNAC. .) (POTENTIAL).
103416 MW; AF6B323BOA4C789D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                     9.7%; Score 179.5; DB 1; Length 928;
31.6%; Pred. No. 2e-07;
ive 29; Mismatches 73; Indels 17;
                                                                                                        NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL)
                                                                                                                                             CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                      F5/8 TYPE C 1.
F5/8 TYPE C 2.
MAM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT; 707 AA
                                                                                                                                                                                                                                                                                                                                                                                                                  ilarity 31.6%; Pred. No. 2e-0
Conservative 29; Mismatches
                                                                                                                                 POTENTIAL.
                                                                                            POTENTIAL
                                                                                                                                                                                                                             PROBABLE.
                                                                                                                                                                                                                                                      PROBABLE
                                                                                                                                                                                                                                                                      PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE=Embryo;
MEDLINE=94085787; PubMed=8262384;
                                                                                                                                                              GGB
; PS01285; PA58C_1; 2.
; PS01286; FA58C_2; 2.
; PS50022; PA58C_3; 2.
; PS00740; MAM_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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1173
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NCBI_TaxID=8355;
                                                                                                                                                                                                                                                                                                                                                  523 5
844 8
928 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                 Receptor; Antigen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BMP1 XENLA
P98070;
                                                                                                                                                                                                                                                                                                                                                                                                                                55;
 PROSITE;
PROSITE;
PROSITE;
PROSITE;
                                                                                                                       DOMAIN
TRANSMEM
                                                                                                                                                                                                                                          DISULFID
                                                                                                                                                                                                                                                                                   DISULFID
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                       PROSITE;
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2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Growth factor; Cytokine, Repeat; Bone, Cartilage; Hydrolase; Protease;
Metalloprotease; EGF-like domain; Zinc; Calcium; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CUB 2. EGF-LIKE, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
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BY SIMILARITY.

ZINC (CATALYTIC) (BY SIMILARITY).

ZINC (CATALYTIC) (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 707;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   36; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       114 -PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGF 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    618 LTSDSKLHGKFCGS-ELPAVITSQYNNMRIBFKSDNTV-SKKGF 659
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
BONE MORPHOGENETIC PROTEIN
METALLOPROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80673 MW; 1B6980D716DC9B8D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9.5%; Score 176; DB 1;
43.3%; Pred. No. 2.9e-07;
tive 15; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
-!- SIMILARITY: Contains 1 BGF-like domain.
-!- SIMILARITY: Contains 3 CUB domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POTENTIAL.
                                                                                                                                                                                                                                                                                                         MEROPS; M12.005; AETO, INTERPORS; M12.005; AETO, INTERPORS; M12.005; AETO, INTERPORS; M2.005; AETO, INTERPORS; M2.0015; M3.0015; M3.0015; M3.0015; M3.0015; M3.0015; M3.0015; M3.0017; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUB 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS01180; CUB; 3.
PROSITE; PS00010; ASX HYDROXYL; 1.
PROSITE; PS00021; EGF 1; FALSE NEG-PROSITE; PS01186; EGF 2; 1.
PROSITE; PS01187; EGF CA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COB 1
                                                                                                                                                                                                                                            EMBL; L12249; AAA16313.1; -. PIR; JC2218; JC2218.
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ACT SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
MEDLINE-92315921; Pubmed=1618141;
Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C.;
Reynolds S.D., Angerer L.M., Palis J., Nasir A., Angerer R.C.;
"Early mRNAs, spatially restricted along the animal-vegetal axis of sea urchin embryos, include one encoding a protein related to tolloid
                                                                                                                                     Strongylocentrotus purpuratus (Purple sea urchin).
Bukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
                                                                                                                                                                                                                                                                                                                         Development 114:769-786 (1992).
-!- TISSUE SPECIFICITY: ASYMMETRICALLY ALONG THE ANIMAL-VEGETAL AXIS
OF THE BLASTULA.
                                                                                                                                                                                                                                                                                                                                                                                -!- DEVELOPMENTAL STAGE: VERY EARLY BLASTULA (BETWEEN 16-CELL STAGE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00022; EGF_1; 1.
PROSITE; PS01186; EGF_2; PALSE_NEG.
Developmental protein; Repeat; Hydrolase; Protease; Zinc; Embryo; Metalloprotease; EGF-like domain; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (CATALYTIC) (BY SIMILARITY).
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ACTIVATION PEPTIVE (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ARG/LYS-RICH (BASIC).
                                                                                                                                                                                                                                                                                                                                                                                                          AND MAICHING!
-!- SIMILARIY: BELONGS TO PREFIDASE FAMILY ML2A.
-!- SIMILARIY: Contains 1 BGF-like domain.
-!- SIMILARIY: Contains 2 CUB domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC (CATALYTIC) (
BY SIMILARITY.
ZINC (CATALYTIC) (
ZINC (CATALYTIC)
                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
SPAN protein precursor (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 METALLOPROTEASE
                              616 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001506; Astacin.
InterPro; IPR001506; Astacin.
InterPro; IPR00209; CUB_domain.
InterPro; IPR005109; IEGF_like.
InterPro; IPR006105; NZn WTpeptdse.
InterPro; IPR006025; Zn WTpeptdse.
Flam; PF01400; Astacin; 1.
Pfam; PF00480; AsTacin; 1.
Pfam; PR00480; ASTACIN.
SWART; SW00042; CUB; 2.
SWART; SW00181; EGF; 1.
SWART; SW00181; EGF; 1.
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                              PRT;
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                              STANDARD;
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93
295
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16
93
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                                                                                                                                                                                     Strongylocentrotus.
                                                                                                                                                                                                                                                                                                                                                                                                   AND HATCHING)
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                                                                                                                                                                                                          NCBI_TaxID=7668;
                                                                                                                                                                                                                                                                                                                      BMP-1.";
                              STRPU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SITE
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RESULT 3
SPAN_STRPU
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56 GSIHSPRFPHTYPRNTVLVMRLVAVEENVMIQLTFDERFGLEDPEDDICKYDFVEVEPS 115
                                                                                                                                                                                                                                         116 DGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPS--EPGFCIHYNIVMPQFTEAVSP 173
                                                                                                                                                                                                                                                                174 SVL---PPSALPLDLLNNAITAFSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFG 230
                                                                                                                                                                                                                                                                                                                                                   460 TILQITPPSTITILQITNPSTITILQI-----TNPSTITILQITD--TPVIGSCGGTFV-G 509
                                                                                                                                                                                                                                                                                                                                                                                         231 RKSRVVDLNLLTEEVRLYSCTPRNFSVSIR-----EELKRIDTIF------W 271
                                                                                                                                                                                                   349 GEITSPNYPSNYEDNHACVYBIBGPYGST-IELTF---LDMEIBTETLCRYDAVEVRKDD 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Janitz M., Heiser V., Boettcher U., Landt O., Lauster R.;
"Three alternatively spliced variants of the gene coding for the human
bone morphogenetic protein-1";
J. Mol. Med. 76:141-146 (1998).
                                                                                                                              63; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The C-proteinase that processes procollagens to fibrillar collagens is identical to the protein previously identified as bone morphogenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | BMP1 HUMAN STANDARD; PRT; 986 AA. | PRJ3437; Q13292; Q13423; Q9UL38; P13437; Q13292; Q13872; Q14874; Q99421; Q99422; Q99423; Q9UL38; Q1-37M-1990 (Rel. 13, Created) | 16-OCT-2001 (Rel. 40, Last sequence update) | S4-FEB-2003 (Rel. 41, Last annotation update) | Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1) | Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryoča, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Wozney J.M., Rosen V., Celeste A.J., Mitsock L.M., Whitters M.J., Kriz R.W., Hewick R.M., Wang E.A., "Novel regulators of bone formation: molecular clones and
                                                                                          DB 1; Length 616;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Li S.W., Sieron A.L., Fertala A., Hojima Y., Arnold W.V., Prockop D.J.;
                                                                                                                            70; Conservative 33; Mismatches 93; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. (ISOFORMS BMP1-4; BMP1-5 AND BMP1-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PARTIAL SEQUENCE FROM N.A. (ISOFORMS BMP1-3 AND BMP1-7)
BY SIMILARITY.

BY SIMILARITY.

BY SIMILARITY.

397CD923FFB9EB98 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proc. Natl. Acad. Sci. U.S.A. 93:5127-5130(1996).
                                                                                          9.3%; Score 173.5; DB 27.0%; Pred. No. 3.9e-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORM BMP1-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. (ISOFORM BMP1-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=96209868; PubMed=8643539;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=89072730; PubMed=3201241;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE=98160316; PubMed=9500680;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    272 PGCLL------VKRCG 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        559 DSLMINLGNGIKVGMKMCG 577
 299 315 BY
305 317 BY
319 328 BX
616 AA; 67902 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 242:1528-1534(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sapiens (Human)
                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
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MEDLINE=95096114; PubMed=7798260;
Takahara K., Lyons G.E., Greenspan D.S.;
"Bone morphogenetic protein-1 and a mammalian tolloid homologue (mrld) are encoded by alternatively spliced transcripts which are differentially expressed in some tissues.";
J. Biol. Chem. 269:32572-32578(1994).
                                                                                                                                                                                                                                                              MEDLINE-21336528; PubMed-11283002;

Garrigue-Antar L., Barker C., Kadler K.B.;

"Identification of amino acid residues in bone morphogenetic

"Identification of amino acid residues in bone morphogenetic

"Identification of amino acid residues in bone morphogenetic

"Identification of amino acid residues in bone

"Inportant for procollagen C-proteinase activity.";

"Inportant for procollagen C-proteinase activity.";

"Inportant for procollage Reportation of PROCOLLAGEN I, II

"INDUCES CARTINITY: Cleavage of the C-terminal propeptide at

Ala-|-Asp in type I and II procollagens and at Arg-|-Asp in type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-ENDOPEPTIDASE ENHANCER PROTEIN.
-!- ALTERNATIVE PRODUCTS:
Event-Alternative splicing; Named isoforms=7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INCLAPIA 97-6; Sequence=VSP 005469, VSP 005470; INCLAPIA SPECIFICITY: Ubiquitous.
--- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
--- SIMILARITY: Contains 2 EGF-like domains.
--- SIMILARITY: Contains 5 CUB domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P13497-2; Sequence=VSP_005461, VSP_005462;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=P13497-3; Sequence=VSP_005463, VSP_005464;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=P13497-4; Sequence=VSP_005465, VSP_005466;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=P13497-5; Sequence=VSP_005467, VSP_005468;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MIM. 11264; --

GO; GO: 0006576; C: extracellular; NAS.

GO; GO: 0006277; F: metallopeptidase activity; NAS.

GO; GO: 0001502; F: cartilage condenation; TAS.

GO; GO: 0007275; P: development; TAS.

InterPro; IPRO01505; Astacin.

InterPro; IPRO01505; Astacin.

InterPro; IPRO01805; Astacin.

InterPro; IPRO01805; EGF Like.

InterPro; IPRO06029; EGF Like.

InterPro; IPRO06026; NZn WIPeptdse.

InterPro; IPRO06025; Zn MTPeptdse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Name=BMP1-2;
Isold=P13497-7; Sequence=Not described;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=P13497-1; Sequence=Displayed;
                                                                                                                                                                                                                                          DISULFIDE BOND IN METALLOPROTEASE DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL, U50330; AAA93462.1; BMBL, M22488; AAA5183.1; BMBL; Y08723; CAA69973.1; BMBL; Y08725; CAA69975.1; BMBL; Y08725; CAA69975.1; BMBL; L35278; AAC41703.1; BMBL; A37278; B58788. HSSP, P07736; LAQ, MEROPS; M12.005; CAA69078; C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=BMP1-3;
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DKDECSKDNGGCQQDCVNTFGSYECQCR -> EKRPALQPP
RGRPHQLKFRVQKRNRTPQ (in isoform BMP1-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QEVNFLKMEFQEVESLGETYDFDSIMHYARNTFSRGIFLDT
IVPKYEVNGVKPPIGQR -> VLASSLLLLSCGSRNGASFP
CSLESSTHQALCWTGLFLRPSPFPRLPLAAPRTLRAGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -> GCY
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                                                                                                                                                                                                                                     EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL). CUB 4.
                                                                                                                                                                                                                       EGF-LIKE 1, CALCIUM-BINDING (POTENTIAL) .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DKDECSKDNGGCQQD -> GGELFGLLGHPPRRP (in isoform BMP1-6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (in isoform BMP1-4).
/FTId=VSP 005463.
Missing (in isoform BMP1-4).
/FTIG=VSP_005464.
AAGGGFLTKLNGSITSPGWPKBYPPNKNCIWQLV -
DLQVGKPLLWDRHCFRLSTHGPEMLGTALRG (in
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N-LINKED (GLCNAC. . .) (POTENTIAL)
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BY SIMILARITY.
ZINC (CATALYTIC) (BY SIMILARITY).
                                                                  PROSITE, P800142; ZINC_PROTEASE; 1.
PROSITE; P800180; CUB; 5.
PROSITE; P800101 ASX HYDROXYL; 2.
PROSITE; P800102; EGF_1; FALSE_NEG.
PROSITE; P8001186; EGF_2; 2.
Growth factor; Cytokine; Repeat; Bone; Cartilage; Hydrolase; Metalloprotease; EGF_1ke domain; Zinc; Calcium; Signal; Glycoprotein; Zymogen; Alternative splicing.

Glycoprotein; Zymogen; Alternative splicing.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Missing (in isoform BMP1-1). /FIId=VSP_005462.
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Missing (in isoform BMP1-6).
/FTId=VSP 005468.
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Missing (in isoform BMP1-5).
/FTId=VSP_005466.
                                                                                                                                                                                BONE MORPHOGENETIC PROTEIN METALLOPROTEASE.
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ZINC (CATALYTIC)
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                                      SMART; SM00042; CUB; 5.
SMART; SM00179; EGF CA; 2.
SMART; SM00235; ZNMG; 1.
Pfam, PF01400, Astacin; 1. Pfam; PF00431; CUB; 5. Pfam; PF00008; EGF; 2. PRINTS; PR00480; ASTACIN,
                                                                                                                                                               302
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               599 NGSITSPGWPKEYPPNKNCIWOLVAPIQYRISLÓFDFFFIEG----NDVCKYDFVEVRS 653
                            VKLTFMEMDIESQPECAYDHLEVFDGRDAKAPVLGRFCG
--> VLBGADDRHSHLSGGLELLLCPPHALVDYVRAPESALEGD
--> THATHTHYTHYTHYTP AQETCRGPPLGASTLSPQGPHLTLA
PQEGSYLDFWDTHRGDPKPRRRKSLKTFSLTPATFHGIWA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=94229142; PubMed=8174772;
MEDLINE=94229142; PubMed=8174772;
Fukagawa M., Noborus S., Hogan B.L.M., Jones C.M.;
Fukagawa M., Noborus S., Hogan B.L.M., Jones C.M.;
Fukagawa M., Noborus S., Hogan B.L.M., Jones C.M.;
Which is related to the Drosophila dorsoventral gene tolloid and encodes a putative astacin metalloendopeptidase.";
Dev. Biol. 163:175-183(1994).
-!- FUNCTION: CLEAVES THE C-TERMINAL PROPEPTIDES OF PROCOLLAGEN I, II AND II. INDUCES CAPRILAGE AND BONE FORMATION.
-!- CATALYTIC ACTIVITY: Cleavage of the C-terminal propeptide at Ala-|-Asp in type and II procollagens and at Arg-|-Asp in type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- COFACTOR: Binds 1 zinc ion per subunit (By similarity).
-!- ENZYME REGULATION: ACTIVITY IS INCREASED BY THE PROCOLLAGEN C-
ENDOPERTIDASE ENHANCER PROTEIN.
-!- TISSUE SPECIFICITY: AT HIGH LEVELS IN EMBRYONIC MATERNAL DECIDIUM
AND FLOOR PLATE REGION OF THE NEURAL TUBE. LESS IN DEVELOPING
MEMBRANOUS AND THE MESENCHYME OF SPIEEN AND LUNG.
-!- SIMILARITY: EBELONGS TO PEPTIDASE FAMILY MIZA.
-!- SIMILARITY: CONTAINS 2 EGP-like domains.
EAGCDHKVTSTSGTITSPNWPDKYPSKKECTWAISSTPGHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     39; Indels 10; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ol-FEB-1996 (Rel. 33, Created)
Ol-FEB-1996 (Rel. 33, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Bone morphogenetic protein 1 precursor (EC 3.4.24.19) (BMP-1)
(Procollagen C-proteinase) (PCP) (Mammalian tolloid protein) (mTld).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 114 --PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSBPGFCIHY 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              654 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 986;
                                                                                                                                                                          L (in isoform BMP1-7).

| First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | First | Firs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17; Mismatches
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P98063;
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CONFLICT
SEQUENCE
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55 NGSIHSPRFPHTYPRNTVLVWRLVA-VEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE 113
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; Pred. No. 1.7e-06;
17; Mismatches 39; Indels 10; Gaps
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(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
(GLCNAC. .) (POTENTIAL).
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PROSITE; PRO10-25; ALMO, TIME, F.
PROSITE; PRO10-20; ALMO, F.
PROSITE; PRO10-25; BGF 1; PALSE NEG.
PROSITE; PRO1186; EGF 2; 2.
PROSITE; PRO1187; EGF CA; 2.
PROSITE; PRO1187; EGF CA; 2.
PROSITE; PRO10-25; PROPER SEPERT; PROFE; PROF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BONE MORPHOGENETIC PROTEIN 1.
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                                                                                                                                                                                                                              Interpro; IPR006209; EGF_Ca.
Interpro; IPR006209; EGF_like.
Interpro; IPR006209; NZn_Mrpeptdse.
Interpro; IPR006025; Zn_Mrpeptdse.
Pfam; PF01400; Astacin; 1.
Pfam; PF00431; CUB; 5.
Pfam; PF000431; CUB; 5.
PRINTS: Definition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED
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                                                                                                MEROPS; mis.v..;
MEROPS; mis.v.s;
Mach. MG1: 88176; Bmpl.
InterPro; IPR001506; Ask hydroxyl.
InterPro; IPR000152; Ask hydroxyl.
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EMBL; 124755; AAA37306.1; -. PIR; 149540; 149540.
HSSP; P00736; 1APQ.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00480; ASTACIN.
SMART; SM00042; CUB; 5.
SMART; SM00179; EGF_CA; 2.
SMART; SM00235; ZnMC; 1.
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SIGNAL 1 25
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X MEDLINE-20309748; PubMed=10748121;
A Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;
Gluzman-Poltorak Z., Cohen T. Herzog Y., Neufeld G.;
T "Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid form of vascular endothelial growth factor (VEGF) and of placenta T growth factor-2, but only neuropilin-2 functions as a receptor for T the 145-amino acid form of VEGF.";
L J. Biol. Chem. 275:18040-18045(2000).
- PUNCTION: HIGH APFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
- NUN VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
- SUBNIAT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH COMPLEX LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. (ISOFORMS A0 AND A17).
MEDLINE-97470888; PubMed-9331348;
Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
"Neuropilin-2, a novel member of the neuropilin family, is a high
affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                                            NRP2 HUMAN STANDARD; PRT; 931 AA.
060462; 014821;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
18-FBB-2003 (Rel. 41, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.; "Neuropilin-1 is expressed by endothelial and tumor cells as an isoform-specific receptor for vascular endothelial growth factor."; Cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                  Homo sapiens (Human).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
659 GLTADSKLHGKFCGS-EKPEVITSQYNNMRVEFKSDNTV-SKKGFKAHF 705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 180Id=060462-3; Sequence=VSP_004241;
-!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-!- SIMILARITY: Contains Z CUB domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Event=Alternative splicing; Named isoforms=3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IsoId=060462-2; Sequence=VSP_004342;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Name=A22;
Isold=060462-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Breast;
MEDLINE=98188099; PubMed=9529250;
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EMBL; AF022860; AAC51789.1; -.
EMBL; AF016098; AAC12922.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neuron 19:547-559(1997).
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                                                                                                                                                                                                                                                        receptor 2).
NRP2 OR VEGF165R2.
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                                                                                             NRP2_HUMAN
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61 PRFPHTYPRNTVLVWRLVAVBENVWIQLTFDERFGLEDPEDDICKYDFVEVE--EPSDGT 118
GO; GO:0005624; C:membrane fraction; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0004872; F:receptor activity; TAS.
GO; GO:0007411; F:vascular endochelial growth factor receptor. . .; TAS.
GO; GO:0007411; F:axon guidance; TAS.
InterPro; IPR000859; CUB domain.
InterPro; IPR000998; MAM domain.
Pfam; PF00431; CUB; Z: PFE C: 2.
Pfam; PF00529; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
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BY SIMILARITY.
N-LINKED (GLCNAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                        PRINTS; PRO0020; MAMDOMAIN.
SMART; SM000231; FASEC; 2.
SMART; SM000137; MAM; 1.
PROSITE; PS01286; FASEC; 2.
PROSITE; PS01286; FASEC 1; 2.
PROSITE; PS01286; FASEC 2; 2.
PROSITE; PS010202; FASEC 2; 2.
PROSITE; PS00022; FASEC 2; 2.
PROSITE; PS00002; FASEC 2; 2.
PROSITE; PS00000; MAM 2; 1.
Transmembrane; Glycoprotein; Neurone; Signal; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1; Length 931;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           119 ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYPPSEPGFCIHYNI 162
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          809 813 Missing (in isoform A17).
809 830 Missing (in isoform A0).
802 802 FTIG=VSP 004342.
602 602 E -> K (IN REF. 1).
931 AA, 104830 MW; 270CBAE69ADA797C CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CYTOPLASMIC (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NRP1_RAT

ID NRP1_RAT STANDARD; PRT; 922 AA.

AC 090WJG;

DT 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      g
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"Neuropilin is a semaphorin III receptor.";

Cell 90:753-762[1997).

Cell 90:753-762[1997).

Cell 90:753-762[1997).

Cell 90:753-762[1997).

Cell 90:753-762[1997).

Cell 90:753-762[1997).

CERTAIN RECEPTOR INVOLVED IN THE BEVELOPMENT OF THE CARDIOVASCULAR SYSTEM, IN ANGIOCASNESIS, IN THE FORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM.

SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SENAPHORINS. IT BINDS TO SEMAPHORIN 34, THE PLGF-2 ISOPORM OF PGF, THE VEGF-165

INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.

INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.

CHARACTER OF THE NEUROPE TO THE REMBRYONIC NERVOUS SYSTEM.

CHARACTER OF THE NEUROPELIN FAMILY.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstainnthe the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                              Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat;
                                                                                                                                                                                                      STRAIN=Sprague-Dawley;
MEDLINE=97433085; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Rowe B.G., Tai Y.-T., Giger R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
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CYTOPLASMIC (POTENTIAL).
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F5/8 TYPE C 2.
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PROBABLE.
PROBABLE.
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Interpro, IPR000421; FA58 C.
Interpro, IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SMART; SM00042; CBB; 2.
SMART; SM00131; FASEC; 2.
SMART; SM00137; MAM; 1.
PROSITE; PS01180; CBB; 2.
PROSITE; PS01286; FASEC_1; 2.
PROSITE; PS01286; FASEC_2; 2.
PROSITE; PS01286; FASEC_2; 2.
PROSITE; PS00740; MAM 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pfam; PF00431; CUB; 2.
Pfam; PF00754; P5 F8 type C; 2.
Pfam; PF00629; MAM; 1.
PRINTS; PR00020; MAMDOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF016296; AAC53337.1; -.
HSSP; P12259; 1CZT.
                                                                                                                                                                                  SEQUENCE FROM N.A
                                                                                                                                           NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     receptor).
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                                                                                                                                                                                  50 ITVSTNGSIHSPREPHTYPRNTVLVWRLVAVBENVWIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                    Rattus norvegicus (Rat).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                         7; Gaps
                                                                                                                                                                                                                                        110 EV--EBPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                     88 EVIDGENEGGRIMGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEI 140
                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
L6-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
BY SIMILARITY.

BY SIMILARITY.

N.LINKED (GLCCARC. . ) (POTENTIAL).

N.LINKED (GLCNAC. . ) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=Sprague-Dawley;
MEDLINE=974330B5; PubMed=9288754;
Kolodkin A.L., Levengood D.V., Rowe E.G., Tai Y.-T., Giger R.J.,
                                                                                                                              8.8%; Score 163.5; DB 1; Length 922;
                                                                                                                                                         Indels
                                                                                                     103082 MW; CC6F82AD098B0F2E CRC64;
                                                                                                                                             Pred. No. 4.7e-06;
                                                                                                                                                         16; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
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InterPro; IPR000421; FA58 C.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5 F8 type_C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; AF016297; AAC53338.1; -.
                                                                                                                                             36.5%;
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                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                     STANDARD;
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SMART; SM00042; CUB; 2.
           424
150
150
261
300
522
                                                                                                     922 AA;
                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI TaxiD=10116;
                                                                                                                                                        42;
                                                                                                                                                                                                                                                                                                                                                                                                                    receptor 2).
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035276;
                      DISULFID
                                                                                      CARBOHYD
                                                                                                                              Query Match
           DISULFID
                                                 CARBOHYD
                                                                            CARBOHYD
                                                                CARBOHYD
                                                                                                                                               Sest Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                74 PHFEIEKHD---CKYDFIEIRDGDSESADLIGKHCGN-IAPPTIISSGSVLYIKFTSD-Y 128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            32 FSSNKEQNGVQDPQHERIITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLIFD 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15 FSGHKVRS-QODPPCGGRINSKDAGXITSPGYPQDYPSHQNCEWVVYAPEPNQKIVLNFN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               035251;
28-FEB-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
15-SEP-2004 (Rel. 42, Last annotation update)
15-SEP-2005 (Rel. 42, Last annotation update)
16-SEP-2007 (Rel. 42, Last annotation update)
17-SEP-2008 (Rel. 42, Last annotation update)
18-SEP-2009 (Rel. 42, Last annotation update)
18-SEP-2009 (Rel. 42, Last annotation update)
18-SEP-2009 (Rel. 41, Last anno
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                 SMART; SM00137; MAM; 1.

PROSTIE; PS01180; CUB; 2.

PROSTIE; PS01285; FASSC 2; 2.

PROSTIE; PS01286; FASSC 3; 2.

PROSTIE; PS50062; FASSC 3; 2.

PROSTIE; PS50060; MAM 2; 1.

Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.8%; Score 163; DB 1; Length 925;
3.8%; Pred, No. 5.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   60; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    134 N-LINKED (GLCNAC. . .) (POT
103896 MW; 3BF62903F644851C CRC64;
                                                                                                                                                                                                       NEUROPILIN-2.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (GLCNAC. . .)
(GLCNAC. . .)
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                                                                                                                                                                                                                                                                                                                                                                                                            BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
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BY SIMILARITY.
N-LINKED (GLCNAN-LINKED (GLCNAN-LINKED)
N-LINKED (GLCNAN-LINKED)
N-LINKED (GLCNAN-LINKED)
N-LINKED (GLCNAN-LINKED)
                                                                                                                                                                                                                                                                                                                                          F5/8 TYPE C 1.
F5/8 TYPE C 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       33.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               129 ARQGAGFSLRYEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   45; Conservative
SMART; SM00231; FA58C; 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
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834 8
925 AA;
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DOMAIN
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DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    155 GFCIHYNIVMPQFTEAVSPSVLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLED 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           215 LYRPTWQLLGKAFVFGRKSR------VVDLNLLTEEVRLYSCTPRNFSVSIREE 262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   263 L-KRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCV---PSKVTKKYHEVLQLRPKTGVR 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68
activates VEGFR-3 (Flt4) receptor (By similarity).

-I-SUBCNIT: Homodimer; non-covalent and antiparallel (By similarity).

-I-SUBCELLULAR LOCATION: Secreted (By similarity).

-I-PTM: Undergoes a complex proteolytic maturation which generates a variety of processed secreted forms with increased activity toward VEGFR-3 and VEGFR-2. VEGF-D first form an antiparallel homodimer linked by disulfide bonds before secretion. The fully processed VEGF-D is composed mostly of two VEGF homology domains (VHDs) bound by non-covalent interactions (By similarity).

-I-SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 GFSIEHRAVKDVSLERSSRSVLERS-----EQQIRAASTLEELLQVAHSEDWK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 LWRCRLKLKSLANVDSRSTSHRSTRFAATFYDTETLKVIDEEWORTOCSPRETCVEVASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 8.7%; Score 162.5; DB 1; Length 326; Best Local Similarity 30.0%; Pred. No. 1.5e-06; Matches 61; Conservative 23; Mismatches 80; Indels 39; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SMART; SM00141; FUGF 1.
PROSTIE; PS00249; PDGF 1; 1.
ANGIOGENESIS; MILOGEN; Growth factor; Glycoprotein; Signal; Repeat;
Angiogenesis; Mitogen; Growth factor; Glycoprotein; Signal; Repeat;
Cleavage on pair of basic residues; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
VARCULAR ENDOTHELIAL GROWTH FACTOR D.
POTENTIAL.
4 X 16 AA REPEATS OF C-X(10)-C-X-C-X(1,3)-C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-LINKED (GLCNAC, .,) (POTENTIAL).
N-LINKED (GLCNAC, .,) (POTENTIAL).
N-LINKED (GLCNAC, .,) (POTENTIAL).
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INTERCHAIN (BY SIMILARITY).
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4 (INCOMPLETE)
                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR004153; CXCXC_repeat.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00128; CXCXC; 1.
Pfam; PF00341; PDGF; 1.
Proplom; PD001629; PD_growth_factor; 1.
SWART; SM00141; PDGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ---PELVPVKIANHTGCKCLPTG 200
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                                                                                                                                                                                                                                                                                                                                                           EMBL; AF014827; AAB66557.1; -.
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326
317
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326 AA;
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PROPEP
DOMAIN
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RESULT 10

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Theuropilin, in the mouse nervous system...;

1. Neurobiol. 29:1-17(1996).

2. PONCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE CARDIOVASCULAR SYSTEM. IN ANOIOGENESIS. IN THE PORMATION OF CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEARPHORINS. IT BINDS TO SEMAPHORIN 34, THE PLGF-2 ISOPORM OF PGF, THE VEGF-165

INCREASED VEGF-165 BINDING TO KDR AS WELL AS INCREASED CHEMOTAXIS.

IT MAY REGULAR LOCATION: Type I membrane protein.

C. 1- SIMILARITY: BELONGS TO THE NEUROPPILIN FAMILY.

C. 1- SIMILARITY: CONTAINS 2 CUB domains.

C. 1- SIMILARITY: Contains 2 CUB domains.

C. 1- SIMILARITY: Contains 2 FS/8 type C domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the BNED cutstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Remeat;
                                                                                                             Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN=BALB/c; TISSUE=Embryonic brain;
MEDLINE=96553149; PubMed=8748368;
Kawakami A., Kitsukawa I., Takagi S., Fujisawa H.;
"Developmentally regulated expression of a cell surface protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYTOPLASMIC (POTENTIAL).
                            01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last Bequence update)
228-FEB-2003 (Rel. 41, Last amnotation update)
Neuropilin-1 precursor (A5 protein).
923 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F5/8 TYPE C 1.
F5/8 TYPE C 2.
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InterPro; IPR000859; CUB domain.
InterPro; IPR000421; FASE C.
InterPro; IPR000998; MAM Gomain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO0020; MAMDOMAIN.
SNART; SM00042; CUB; 2.
SNART; SM00131; PASSC; 2.
SNART; SM00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01280; PESSC; 2.
PROSITE; PS01286; PESSC; 2.
PROSITE; PS00740; MAM 1: 1.
PROSITE; PS50060; MAM 2: 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; D50086; BAA08789.1; -.
 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           21
923
856
879
923
141
141
424
583
                                                                                                            Mus musculus (Mouse).
                                                                                              NRP1 OR NRP.
 NRP1 MOUSE
P97333;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Receptor.
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4.
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                                                                                                                                                                                                                                                                                                                           31 IKIENPGYLISPGYPHSYHPSEKCEMLIQAPEPYQRIIINFNPHFDLEDRD----CKYDYV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -: ISOId=035375-6; Sequence=VSP 004347;
-: TISSUE SPECIFICITY: EXPRESSED IN DEVELOPING CNS, PNS AND IN SOME NONNEURAL TISSUES INCLUDING LIMB BUDS, DEVELOPING BONES, MUSCLES, INTESTINAL EPITHELIUM, KIDNEY, LUNG AND SUBBANDIBULAK GLAND.
-: DEVELOPMENTAL STAGE: THE EXPRESSION PATTERN IS VERY DYNAMIC AND IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -i- FUNCTION: HIGH AFFINITY RECEPTOR FOR SEMAPHORINS 3C, 3F, VEGF-165
AND VEGF-145 ISOFORMS OF VEGF, AND THE PLGF-2 ISOFORM OF PGF.
-i- SUBUNIT: NEUROPILIN-2 PROBABLY FORMS AN HETEROMERIC COMPLEX WITH
NEUROPILIN-1 IN ORDER TO BE A FUNCTIONAL SEMAPHORIN E RECEPTOR.
-i- SUBCRILULAR LOCATION: Type I membrane protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97470888; PubMed-9331348;
Chen H., Chedotal A., He Z.-G., Goodman C.S., Tessier-Lavigne M.;
"Neuropilin-2, a novel member of the neuropilin family, is a high
affinity receptor for the semaphorins Sema E and Sema IV but not Sema
                                                                                                                                                                                                                                                                      7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                88 EVIDGENEGGRLWGKFCGK-IAPSPVVSSGPFLFIKFVSD-YETHGAGFSIRYEI 140
                                                                                                                                                                                                                                                                                                                                                                          110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYRPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRP2 MOUSE STANDARD; PRT; 931 AA.
035375; 035373; 035374; 035376; 035378;
16-0CT-2001 (Rel. 40, Created)
16-0CT-2001 (Rel. 40, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-2 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                          N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
N-LINKED (GLCNAC. .) (POTENTIAL).
                                                                                                                                                                              103020 MW; 0644B8A170796808 CRC64;
                                                                                                                                                                                                                                   8.6%; Score 160.5; DB 1; Length 923; 36.5%; Pred. No. 8.5e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORMS A0; A17; A22; A5; B0 AND B5).
                                                                                                                                                                                                                                                                      16; Mismatches 50; Indels
                                                                                                                        (GLCNAC. . .)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Event=Alternative splicing; Named isoforms=6;
                                                                                                                N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
                                                                              BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IsoId=035375-4; Sequence=VSP_004343;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IsoId=035375-5; Sequence=VSP_004346;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IsoId=035375-2; Sequence=VSP_004344;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      sold=035375-3; Sequence=VSP_004345;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IsoId=035375-1; Sequence=Displayed;
                           PROBABLE.
PROBABLE.
PROBABLE.
              PROBABLE.
                                                                                                                                                                                                                                                                      42; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neuron 19:547-559(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus (Mouse).
                                                                                                                                                                522
522
842
842
923 AA;
                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=BALB/c;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=A22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Name=A17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        receptor 2).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=B5;
            DISULPID
                                                               DISULFID
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                                                 DISULPID
                                                                                                  DISULFID
                                                                                                                    CARBOHYD
                                                                                                                                   CARBOHYD
                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EDFKVDIPETHGGEGYEDEIDDEYEGDWSNSSSSTSGAGDP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SSGKEKSWLYTLDP1L1T1AMSSLGVLLGATCAGLLLYCT
CSYSGLSSRSCTTLENYNFELYDGLKHKVKINHOKCCSEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -> GTLPPGTEPTVDTVPVQPIPAYWYYVMAAGGAVLVLAS
VVLALVLHYHRFRYAAKKTDHSITYKTSHYTNGAPLAVEPT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                POLY-SER.

BY SIMILARITY.

N-LINKED (GLONAC. ..) (POTENTIAL).

N-LINKED (GLONAC. ..) (POTENTIAL).

N-LINKED (GLONAC. ..) (POTENTIAL).

'TINKED (GLONAC. ..) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ransmembrane, Glycoprotein; Neurone; Signal; Repeat; Receptor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LTIKLEQERGSHC (in isoform B0). /FTId=VSP_004346.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (1882.1.2)
/FITG=VSP 004343.
Missing (In isoform A0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (in isoform A5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CYTOPLASMIC (POTENTIAL).
DEVELOPMENTALLY REGULATED.
SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
SIMILARITY: Contains 2 CUB domains.
SIMILARITY: Contains 2 F5/8 'type C domains.
SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       004345.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 F5/8 TYPE C 1.
F5/8 TYPE C 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COB
                                                                                                                                                                                    EMBL, AF022856, AAC53379.1, -.
EMBL, AF022854, AAC53377.1, -.
EMBL, AF022855, AAC53378.1, -.
EMBL, AF022857, AAC53380.1, -.
EMBL, AF022861, AAC53381.1, -.
                                                                                                                                                                                                                                                                                          InterPro; IPR000859; CUB domain.
InterPro; IPR000421; FA58 C.
InterPro; IPR000998; MAM_domain.
                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00020; MAMDOMAIN.
SMART; SM00042; CUB; 2.
SMART; SM01012; FASSC; 2.
SMART; SM01017; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FASSC 1; 2.
PROSITE; PS01285; FASSC 2; 2.
PROSITE; PS50022; FASSC 3; 2.
PROSITE; PS50060; MAM 2; 1.
                                                                                                                                                                                                                                                                                                                                  Pfam; PF00431; CUB; 2.
Pfam; PF00754; F5_F8_type_C; 2.
Pfam; PF00629; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  931
                                                                                                                                                                                                                                                                                MGI:1100492; Nrp2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Alternative splicing
                                                                                                                                                                                                                                                        AF022861; AA(
P12259; 1CZT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  810
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DOMAIN
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                                                                                                                                                                                                                                                                                                 1 MSLFGLLLVTSALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS 60
                                                                                                                                                                                                                                                                                                                                          FUNCTION, AND TISSUE SPECIFICITY.

**MEDILINE=99307076; PUNC## PA:0.3 **.

**Comnors S.A., Trout J., Parker M., Mullins M.C.;

"The role of tolloid/mini fin in dorsoventral pattern formation of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development 126:3119-3130(1999).

-!- FUNCTION: Required for patterning ventral tissues of the tail. May increase bone morphogenetic procein (BMP) activity at the end of gastrulation by proteolytic cleavage of chordin and release of BMP from inactive complexes.

-!- TISSUE SPECIFICITY: During gastrulation, accumulates around the
                    EKSMLYTLDPILITIIAMSSLGVLLGATCAGLLLYCTCSYS
GLSSRSCTTLENYNFELYDGLKHKVKINHQKCCSEA -> G
GTLPPGTEPTVDTVPVQPIPAYWYYWAAGGAVLVLASVVL
                                                                               ALVLHYHRPRYAAKKTDHSITYKTSHYTNGAPLAVEPTLTI
KLEQERGEHC (in isoform B5).
FTTd=vSP_004347.
FTTd=vSP_004347.
786 G -> I (IN REF. 1; AAC53380/AAC53381).
104558 MW; 76F2443F411D2F63 CRC64;
VDIPETHGGEGYEDEIDDEYEGDWSNSSSSTSGAGDPSSGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                closing blastopore with greater expression ventrally. At the animal pole, expressed in the ectoderm flanking the anterior neural plate. At the 10-semite stage, expressed in the developing tailbud and cranial neural crest. At the 20-semite stage, also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Blader P., Rastegar S., Fischer N., Straehle U.; "Cleavage of the BMP-4 antagonist chordin by zebrafish Tolloid."; Science 278:1937-1940(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001 (Rel. 40, Created)
LoCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last amoretion update)
Dorsal-ventral patterning tolloid protein precursor (EC 3.4.24.-)
                                                                                                                                                                                                              8.6%; Score 160.5; DB 1; Length 931;
10.5%; Pred. No. 8.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 LLGKHCGN-IAPPIIISSGSVLYIKFTSD-YARQGAGFSLRYEI 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         119 ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressed in the hematopoietic system.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M12A.
-!- SIMILARITY: Contains 2 EGF-like domains.
-!- SIMILARITY: Contains 5 CUB domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT; 1022 AA.
                                                                                                                                                                                                                                                           50; Conservative 18; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=98057457; PubMed=9395394;
                                                                                                                                                                                                                                       30.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
    931
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Mini fin protein).
TOLLOID OR TLD OR MFN.
                                                                                                                                                                                                                                       est Local Similarity
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    814
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    VARSPLIC
                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                  Query Match
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TLD BRARE
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRINTS, PRO0009, ASTACIN.
SMART; SM00042; CUB; 5.
SMART; SM00042; CUB; 5.
SMART; SM00019; BGF_CA; 2.
SMART; SM00139; ABC, CA; 2.
PROSITE; PS00100, ASX_HYDROXYL; 2.
PROSITE; PS01186; EGF 1; FALSE_NEG.
PROSITE; PS01186; EGF 2; 2.
PROSITE; PS01187; EGF 2; 2.
PROSITE; PS01147; ZING_PROTEASE; 1.
Developmental protein; Hydrolase; Protease; Metalloprotease; Zinc; Metal-binding; Calcium; EGF-like domain; Repeat; Signal; Glycoprotein;
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N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
N-LINKED (GLCNAC. . ) (POTENTIAL).
L15536 MW; A68CAIDD641793F9 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       METALLOPROTEASE (BY SIMILARITY).
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EGF-LIKE 1, CALCIUM-BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EGF-LIKE 2, CALCIUM-BINDING (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (CATALYTIC)
(CATALYTIC)
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ZINC (CATALYTI
ZINC (CATALYTI
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                                                                                                                                                                                                                                         ZFIN, ZDB-GENR-990415-265; tolloid. InterPro; IPR001506; Astacin. InterPro; IPR001506; Astacin. InterPro; IPR001801; Ast Mydraxyl. InterPro; IPR001881; EGF Ca. InterPro; IPR006809; EGF ZA. InterPro; IPR006809; EGF ZA. InterPro; IPR006025; Zn WIPSPtdse. Pfam; PF01400; Astacin; I. Pfam; PF01401, Astacin; I. Pfam; PF00401; GUB; 5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZINC
                                                                                                                                                                   EMBL; AF027596; AAC60304.1; -. HSSP; P35555; 1EMN.
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156
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Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;

Gluzman-Poltorak Z., Cohen T., Herzog Y., Neufeld G.;

"Neuropilin-2 and neuropilin-1 are receptors for the 165-amino acid
form of vascular endothelial growth factor (VEGF) and of placenta

growth factor-2, but only neuropilin-2 functions as a receptor for
the 145-amino acid form of VEGF."

J. Biol. Chem. 275:18040-18045(2000)

C. !- FUNCTION: The membrane-bound isoform 1 is a receptor involved in
the development of the cardiovascular system, in anglogenesis, in
the development of certain neuronal circuits and in organogenesis
cutside the nervous system. It mediates the chemorepulsant
activity of semaphorins. It binds to semaphorin 3A, The PLGF-2
isoform of PGF, The VEGF-165 isoform of VEGF and VEGF-16.
Coexpression with KDR results in increased VEGF-165 binding to KDR
as well as increased chemotaxis. It may regulate VEGF-induced
                                             9
                                                                                     55 NGSIHSPREPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEE- 113
                                                                                                               TISSUE=Prostatic adenocarcinoms, MEDLINE=20183929; PubMed=10688880; Gagnon M.L., Bielenberg D.R., Gechtman Z., Miao H.-Q., Takashima S., Soker S., Klagsbrun M.; Ucchification of a natural soluble neuropilin-1 that binds vascular endothelial growth factor: In vivo expression and antitumor
                                             8; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Soker S., Takashima S., Miao H.-Q., Neufeld G., Klagsbrun M.;
"Neuropilin-1 is expressed by endothelial and tumor cells as an
isoform-specific receptor for vascular endothelial growth factor.";
cell 92:735-745(1998).
                                                                                                                                                                                                                                                                                                                                       NRP1_HUMAN STANDARD; PRT; 923 AA.
014786; 060461;
30-MAY-2000 (Rel. 39, Created)
16-CT-2001 (Rel. 40, Last sequence update)
15-SEP-2003 (Rel. 42, Last annotation update)
Neuropilin-1 precursor (Vascular endothelial cell growth factor 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Neuropilin is a receptor for the axonal chemorepellent semaphorin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: The soluble isoform 2 binds VEGF-165 and appears to inhibit its binding to cells. It may also induce apoptosis by sequestering VEGF-165. May bind as well various members of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens (Human).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Buteleostomi;
Mammalia, Butheria, Primates; Catarrhini, Hominidae, Homo.
                                                                                                                                                                             114 -PSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHY 160
                                                                                                                                                                                                         Query Match 8.6%; Score 159; DB 1; Length 1022; Best Local Similarity 39.8%; Pred. No. 1.3e-05; Matches 43; Conservative 19; Mismatches 38; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 1), AND SEQUENCE OF 22-39.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. (ISOFORM 2), AND SEQUENCE OF 22-31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             activity.";
Proc. Natl. Acad. Sci. U.S.A. 97:2573-2578(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=20309748; PubMed=10748121;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE=97433084; PubMed=9288753;
He Z., Tessier-Lavigne M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=98188099; PubMed=9529250;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRP1 OR NRP OR VEGF165R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cell 90:739-751(1997).
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Name=1; Synonyms=Membrane-bound;

IsoId=014786-1; Sequence=Displayed;

Name=1; Synonyms=Soluble, SNRP1;

IsoId=014786-2; Sequence=VSP 00439, VSP 004340;

In Independent of the nervous system. In adult tissues, it is highly expressed in heart and placentes; moderately in lung, liver, skeletal muscle, kidney and pancreas; and low in adult brain.

Isoform 2 is found in liver hepatocytes, kidney distal and proximal tubules.
                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the SWIL outstation the Buropean Bloinformatics Institute. There are no restrictions on its use by non-profit institutions along as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MIM, 602069; -.
GO, GO:0005021; F:vascular endothelial growth factor receptor. . .; TAS.
GO; GO:000741; P:axon guidance; TAS.
GO; GO:0007267; P:cell-cell signaling; TAS.
GO; GO:0007397; P:histogenesis and organogenesis; TAS.
GO; GO:0007397; P:histogenesis and organogenesis; TAS.
GO; GO:0007365; P:signal transduction of cell proliferation; TAS.
GO; GO:0007165; P:signal transduction, TAS.
InterPro; IPR000829; GUB domain.
InterPro; IPR000989; MAM Gomain.
Prop: IPR001398; MAM Gomain.
Prop: IPR00131; FS FS L.
Pfam; PF00529; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FIGURES PRODOCS | MAMDONAIN.
SMART; SMO0042; CUB; 2.
SMART; SMO0042; CUB; 2.
SMART; SMO0131; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; PA58C_1; 2.
PROSITE; PS0022; PA58C_2; 2.
PROSITE; PS00740; MAM 1; 1.
PROSITE; PS00740; MAM 1; 1.
PROSITE; PS0060; MAM 2; 1.
semaphorin family. Its expression has an averse effect on blood
vessel number and integrity.
-!- SUBCELLULAR LOCATION: Type I membrane protein. Isoform 2 is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL. CYTOPLASMIC (POTENTIAL)
                                                                                                                                                                                                                                                          -!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-!- SIMILARITY: Contains 2 CUB domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 1 MAM domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F5/8 TYPE C 1.
F5/8 TYPE C 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MAM.
PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL, AF018956; AAC51759.1; -.
EMBL, AF016060; AAC12921.1; -.
EMBL, AF145712; AAF44344.1; -.
PDB; 1KEX; 28-JAN-03.
                                                          -!- ALTERNATIVE PRODUCTS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genew; HGNC:8004; NRP1.
MIM; 602069; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
DOMAIN
DISULFID
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
TRANSMEM
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 50 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         31 İKIESPGYLTSPGYPHSYHPSEKCEWLIQAPDPYQRİMINFNPHFDLEDRD---CKYDYV 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             developing chick nervous system.";
Dev. Biol. 170:207-222(1995).
-!- FUNCTION: RECEPTOR INVOLVED IN THE DEVELOPMENT OF THE
CARDIOVASCULAR SYSTEM, IN ANGIOGENESIS, IN THE FORMATION OF
CERTAIN NEURONAL CIRCUITS AND IN ORGANOGENESIS OUTSIDE THE NERVOUS
SYSTEM. IT MEDIATES THE CHEMOREPULSANT ACTIVITY OF SEMAPHORINS (BY
SIMILARITY). SEEMS TO HAVE CALCIUM-INDEPENDENT CELL ADHESION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
STRAIN=White leghorn; TISSUE=Embryonic brain;
MEDLINE=99324761; PubMed=7601310;
Takagi S., Kasuya Y., Shimizu M., Matguura T., Tsuboi M., Kawakami A.,
Fujisawa H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gallus gallus (Chicken).
Eukaryota, Metazoa, Chordata; Craniata; Vertebrata, Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNI 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88 EVEDGENENGHFRGKFCGK-IAPPPVVSSGPFLFIKFVSD-YETHGAGFSIRYEI 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       O.F
                                                                                                    D 150 150 N-LINKED (GLCNAC. . .) (POTENTIAL).
D 261 261 N-LINKED (GLCNAC. . .) (POTENTIAL).
D 300 300 N-LINKED (GLCNAC. . .) (POTENTIAL).
D 522 522 N-LINKED (GLCNAC. . .) (POTENTIAL).
C 642 842 N-LINKED (GLCNAC. . .) (POTENTIAL).
C 644 EFP - 5 GIK (in isoform 2).
FTIG=VSP 004319.
C 645 923 Missing (in isoform 2).
FTIG=VSP 004319.
FTIG=VSP 004319.
T 26 26 K -> B IN REF. 1).
T 79 749 749 D -> H (IN REF. 2).
T 855 855 E -> D (IN REF. 2).
E 923 AA, 103120 NW; ADEADC4A849E5D57 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- TISSUE SPECIFICITY: DEVELOPING NERVOUS SYSTEM; OPTIC TECTUM
(LAYERS D AND B OF SGFS), AMAGKINE CELLS OF RETINA, NEURITES OF
DORSAL ROOT GANGLIA. ALSO EXPRESSED IN NONNEURONAL CELLS, E.G.
BLOOD VESSELS IN THE ENTIRE EMBRYO.
-!- SIMILARITY: BELONGS TO THE NEUROPILIN FAMILY.
-!- SIMILARITY: Contains 2 CUB domains.
-!- SIMILARITY: Contains 2 F5/8 type C domains.
-!- SIMILARITY: Contains 1 FAAM domain.
                                                                                                                                     (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   8.5%; Score 158.5; DB 1; Length 923; 35.7%; Pred. No. 1.3e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Expression of a cell adhesion molecule, neuropilin, in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              49; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Last sequence update)
28-FEB-2003 (Rel. 41, Last annotation update)
Neuropilin-1 precursor (A5 protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Mismatches
                                                     BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
173
228
228
150
150
300
522
644
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=9031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROPERTIES.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NRP1 CHICK
P79795:
DISULFID
DISULFID
DISULFID
DISULFID
                                                                                                                                                                                                                           CARBOHYD
                                                                                                             CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                           VARSPLIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 14
NRP1_CHICK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
    COC SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SERVICE SE
      use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an enail to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50 ITVSTNGSIHSPRFPHTYPRNTVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFV 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110 EV--EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVM--P 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          166 Q----FTEAVSPSVLP--PSALPLDL-----LINNAITAFSTLEDLIRYLEPE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 ECSRNFTSSSGMIKSPGFPEKYPNSLECTY11FAPKMSEIILEFESFE----LEPD 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PCOL HUMAN STANDARD; PRT; 449 AA.
(1513; O14550;
30-MAY-2000 (Rel. 39, Created)
10-MAY-2000 (Rel. 39, Last sequence update)
115-SEP-2003 (Rel. 42, Last amnotation update)
Procollagen C-proteinase enhancer protein precursor (PCPE) (Type I procollagen COGH-terminal proteinase enhancer) (Type I procollagen COGH-terminal proteinase enhancer) (Type I procollagen COGH-terminal proteinase enhancer)
    institutions as long as its content is in no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                68; Indels 30; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Angiogenesis; Transmembrane; Glycoprotein; Neurone; Signal; Repeat; Receptor; Cell adhesion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 157; DB 1; Length 914; Pred. No. 1.7e-05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BY SIMILARITY.
BY SIMILARITY.
1; DD2EE6D6F0CBB68C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NEUROPILIN-1.
EXTRACELLULAR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE C 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROBABLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROBABLE.
PROBABLE.
                                                                                                                            HSS; P12259; ICCT.
InterPro; IPR000859; CUB_domain.
InterPro; IPR000421; PA58 C.
InterPro; IPR000998; MAM_domain.
Pfam; PF00431; CUB; 2.
Pfam; PF00159; MAM, Trype_C; 2.
Pfam; PF00629; MAM; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    F5/8
                                                                                                                                                                                                                                                                                                                             SMART; SW00137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FA58C_1; 2.
PROSITE; PS01026; FA58C_2; 2.
PROSITE; PS00022; FA58C_3; 2.
PROSITE; PS00740; MAM 1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102480 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    8.4%;
                                                                                                      EMBL; D45416; BAA08256.1; -.
                                                                                                                                                                                                                                                                 PRINTS; PR00020; MAMDOMAIN.
                                                                                                                                                                                                                                                                                   SMART; SM00042; CUB; 2.
SMART; SM00231; FA58C; 2.
SMART; SM00137; MAM; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              914 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISULFID
DISULFID
SEQUENCE
                                                                                                                                                                                                                                                                                                                           SMART; SM
PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RANSMEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
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      OSSIGNATION
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"Type I procollagen COOH-terminal processions consistent of the identification, primary structure, and chromosomal localization of the cognate human gene (PCOLCE).";
J. Biol. Chem. 269:26280-26288 (1994).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Post-translational proteolytic processing of procollagen C-terminal proteinase enhancer releases a metalloproteinase inhibitor."; J. Biol. Chem. 275:1384-1390(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Large-scale sequencing of two regions in human chromosome 7q22: analysis of 650 kb of genomic sequence around the EPO and CUTL1 loci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mott J.D., Thomas C.L., Rosenbach M.T., Takahara K., Greenspan D.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-99134301, PubMed-9933570; Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.; Scott I.C., Clark T.G., Takahara K., Hoffman G.G., Greenspan D.S.; "Structural organization and expression patterns of the human and mouse genes for the type I procollagen COOM-terminal proteinase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDINE=99018118; PubMed=9799793;
Gloeckner G., Scherer S., Schattevoy R., Boright A.P., Weber J.,
Tsui L.-C., Rosenthal A.;
                                                                                                                         Takahara K., Kessler B., Binlaminov L., Brusel M., Eddy R.L., Jani-Sait S., Shows T.B., Greenspan D.S., "Type I procollagen COOH-terminal proteinase enhancer protein:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PARTIAL SEQUENCE, AND CHARACTERIZATION OF INHIBITORY ACTIVITY. MEDLINE-20092917; PubMed=10625689;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                          Unpublished observations (FEB-2000).
                                                                                IISSUE=Placenta;
MEDLINE=95014462; PubMed=7523404;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genome Res. 8:1060-1073(1998).
                                                                                                                                                                                                                                                                                                                        REVISIONS TO 56; 154 AND 373.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 enhancer protein.";
Genomics 55:229-234(1999).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                  SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             reveals 17 genes.
WCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           TISSUE=Heart;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Banda M.J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 56 GSIHSPREPHT-YPRNTVLVWRLVAVEENVWIQLIFDERFGLEDPEDDICKYDFVEV--- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                112 EEPSDGTILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSEPGFCIHYNIVMPQFT--- 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         224 AVSDDSRRLGKFCGD-AVPGSISSEGNELLVQFVSDLSVTAD-GFSASYK-TLFRGTAKE 280
-!- FUNCTION: BINDS TO THE COCH-TERMINAL PROPERTIDE OF TYPE I PROCOLLAGEN AND EMFANCES PROCOLLAGEN C-PROTEINASE ACTIVITY.
-!- FUNCTION: C-TERMINAL PROCESSED PART OF PCPE (CT-PCPE) MAY HAVE AN METALLOPROTEINASE INHIBITORY ACTIVITY.
-!- SUBCELLULAR LOCATION: Secreted.
-!- PIPM: C-TERMINALLY PROCESSED AT MULTIPLE POSITIONS.
-!- SIMILARITY: Contains 2 CUB domains.
-!- SIMILARITY: Contains 1 NTR domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          50; Indels 22; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLEAVAGE.
CLEAVAGE.
CLEAVAGE.
CLEAVAGE.
CLEAVAGE.
CLEAVAGE.
CLEAVAGE.
N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
W; 3D88430158648796 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROCOLLAGEN C-PROTEINASE ENHANCER PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 449;
                                                                                                                                                                                                                                                                                                                                            MIM; 600270; -.
GO; GO:0008151: P:cell growth and/or maintenance; TAS.
GO; GO:0007275; P:development; TAS.
GO:0007275; P:development; TAS.
InterPro; IPR000859; CUB domain.
InterPro; IPR001134; Netrin_C:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8.3%; Score 154; DB 1;
33.8%; Pred. No. 1.2e-05;
tive 22; Mismatches 50;
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                                                                                                                                                                                                                                      EMBL, L33799; AAA61849.1; ALT SEC.
EMBL, ABC08549; BAA32811; --
EMBL, AFC63356; AAC78800.1; --
EMBL, BC00574; AAD16041.1; --
EMBL, BC00574; AAH00574.1; --
EMBL, BC03205; AAH33205.1; --
GMIN, 600270; --
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Pfam; PF0159; NTR; 1.
SMART; SM00643; C345C; 1.
SMART; SM00042; CUB; 2.
PROSITE; PS01180; CUB; 2.
Glycoprotein; Repeat; Signa
SIGNAL
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Best Local Similarity
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2829
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449 AA;
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(without alignments)
2922.663 Million cell updates/sec
                                                                                November 25, 2003, 20:58:59 ; Search time 30.4613 Seconds
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1858
1 MSLFGLLLVTSALAGQRRGT......DVALEHHEECDCVCRGSTGG 345
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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sp_phage:*
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sp_rodent:*
sp_virus:*
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sp_vertebrate:*
sp_unclassified:*
sp_vertebrate:*
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Gapop 10.0 , Gapext 0.5
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Q99Jm4 mus musculu		070244 rattus norv	Opwame mus musculu	O57381 xenopus lae	Ogna00 nomo sapien	Q9y617 homo sapien	Q9z135 rattus norv	ninsenm snm 0zdq80	OBGZY7 mus musculu	O9h2e2 homo sapien	omou	O9h2d5 homo sapien	omou-	Q9h2e3 homo sapien	09qx38 rattus norv	Ostu53 canis tamil	Q8ji28 xenopus Lae	096190 homo sapien	096ih5 homo sapien	Q9h2el homo saplen	Osuvro gallus gall		Obder7 gallus gall	Q9ukz9 homo sapien	057382 xenopus tae	091ze4 rattus norv	Q9brh3 homo sapien
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182	180	176	176	172	171	171	171	169	165.5	165.5	164.5	164.5	164.5	164.5	164.5	163.5	163.5	161.5	158.5	158.5	158.5	157.5	157.5	157	153	153	151.5	151
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ALIGNMENTS

345 AA

PRT;

PRELIMINARY;

RESULT 1 Q9NRA1 ID Q9NRA1

Gaps Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo. TISSURE-Lung)

MEDLINE-2026&201; PubMed=10806482;

Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,

Backstrom G., Hellstrom M., Bostrom H., Li H., Soriano P.,

Backstrom G., Heldin C.-H., Alitalo K., Ostman A., Eriksson U.;

PDGF-C is a new protease-activated ligand for the PDGF alphareceptor.";

Met Cell Biol. 2:302-309(2000).

-I. SIMILARITY: CONTAINS 1 CUB DOMAIN.

EMBL, AF244813; AAP80597.1;

Genew, HGNC:8801; PDGFC. ö 100.0%; Score 1858; DB 4; Length 345; 100.0%; Pred. No. 4.1e-172; tive 0; Mismatches 0; Indels 0; UB; 1. DGF 2; 1. 39043 MW; 590889CEASSCCSEA CRC64; 01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Platelet-derived growth factor C. InterPro; IRR000859; CUB_domain.
InterPro; IRR000072; PD_growth_factor.
Pfam; PF0041; CUB; 1.
Pfam; PF00341; PDGF; 1.
SWART; SW00042; CUB; 1. Conservative PROSITE; PS01180; CUB; PROSITE; PS50278; PDGF Homo sapiens (Human) Best Local Similarity Matches 345; Conserva 345 AA; SEQUENCE FROM N.A. NCBI_TaxID=9606; SEQUENCE Query Match Q9NRA1; SO DR REAL REAL BOOK ON THE REAL BOOK ON

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Mus musculus (Mouse)
                                                  Best_Local Similarity
Matches 343; Conserv
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                                                                                                                                                                                          241 LTEEVRLYSCTPRNFSVSIREELKRIDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPSK 300
                     1 MSLPGLLLVTSALAGORRGTQAESNLSSKPOPSSNKEQNGVQDPQHERIITVSTNGSIHS 60
  9
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MEDLINE=20117014; PubMed=10858496;
Hamada I., Ui-Tei K., Miyata Y.;
Hamada I., Ui-Tei K., Miyata Y.;
"A novel gene derived from developing spinal cords, SCDGF, is a unique member of the PDGF/VEGF family.";
PEBS Lett. 475:97-102(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=21347863; PubMed=11297552; M. Kelly J.D., Sheppard P.O., Gilbertson D.G., Duff M.B., West J.W., Kelly J.D., Sheppard P.O., Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M., Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.; "Platelet-derived Growth Factor C (FDGF-C), a Novel Growth Factor That
1 MSLFGLLLVTSALAGORRGTQAESNLSSKFQFSSNKEQNGVQDPQHERIITVSTNGSIHS
                                                                                                                               181 LPLDILINNAITARSTLEDLIRYLEPERWOLDLEDLYRPTWOLLGKAFVFGRKSRVVDLNL
                                                                                                                                                                                                                                                                                                       01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2003 (TrEMBLrel. 23, Last annotation update)
Secretory growth factor-like protein FALLOTEIN (SPINAL CORD-derived HSCDGF OR PDGFC.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tsal Y.J., Lee R.K.K., Lin S.P.; "Fallotein, a novel growth factor like gene identified in human
                                                                                                                                                                                                                    301 VTKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEECDCVCRGSTGG 345
                                                                                                                                                                                                                              Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                     STRAIN=CS7BL/6J;
Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
Gilbertson D., West J., O'Hara P.J.;
Flatelet-derived growth factor C (PDGF-C), a novel growth factor that
binds to PDGF alpha receptor.";
Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 LPLDLLNNAITARSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSRVVDLNL
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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Tsal Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
Tendra cloning of fallotein from mouse ovary.";
Submitted (JAN-1999), to the EMBL/GenBank/DDBJ databases.
                                                                                               99.6%; Score 1851; DB 4; Length 345; 99.4%; Pred. No. 1.9e-171; tive 2; Mismatches 0; Indels C
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PROSITE; PS01180; CUB; 1.
PROSITE; PSS0278; PDGF 2; 1.
SEQUENCE 345 AA; 39029 MW; CDE9E51F40633B78 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Fallotein (Platelet-derived growth factor C).
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                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
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STRAIN=Wister; TISSUE=Kidney;

MEDLINE=21092670; PubMed=11162582;

MEDLINE=21092670; PubMed=11162582;

A Hamada T., UirTei K., Imaki J., Miyata Y.;

Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to SCDGF/POBC-C/fallotein.";

Eschem. Biochwys. Ree: Commun. 280:733-737(2001).

--- SIMILARITY: CONTAINS 1 CUB DOMAIN.

--- SIMILARITY: CONTAINS 1 CUB DOMAIN.

REMB1, AB03830; BBB1969.1;

RINCEPPO; IPRO00072; PD_Growth_factor.

REPEAM: PRO0341; CUB; 1.

SMART; SM00042; CUB; 1.

SMART; SM00041; PDGF; 1.

REMART; SM01041; PDGF; 1.
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85.5%; Pred. No. 1.7e-151;
ive 30; Mismatches 20; Indels 0.
                                                                                                                                                                                                                                                                             01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal cord-derived growth factor.
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Matches 295; Conservative
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Wakaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
NGBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 86.7%; Pred. No. 3e-153;
Matches 299; Conservative 28; Mismatches 18; Indels 0;
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Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; BC037696; ARH37696.1; -
SEQUENCE 345 AA; 38741 MW; 9ASBAOSCGCOE9614 CRC64;
                                                                                                                                                                                                 PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 345 AA; 38741 MW; 3AS8A1F701B84EA2 CRC64;
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01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
platelet-derived growth factor, C polypeptide.
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EMBL; AK042767; BAC31358.1; -.
EMBL; AK052947; BAC35216.1; -.
MGD; MGI:1859631; PGgfc...
InterPro; IPR000859; CUB domain.
InterPro; IPR000072; PD_growth_factor.
Pfam; PF00431; CUB; 1.
SWART; SM00042; CUB; 1.
SWART; SM00141; PDGF; 1.
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Best Local Similarity 86.4%
Matches 298; Conservative
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STRAINS—2017014; PubMed=10858496;

Hamada T., Ui-Tei K., Miyata Y.;

Faranta Gerived from developing spinal cords, SCDGF, is a unique member of the PDGF/VGGF family.";

FEBS Lett. 475:97-102(2000).

FEBS Lett. 475:97-102(2000).

FEBS Lett. 475:97-102(2000).

INTERPRO PROSONOSS CUB Gomain.

InterPro; IPRO00859; CUB Gomain.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
                                                                                                                                   валлы удллы (слискел).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                86.9%; Score 1614; DB 13; Length 345; 83.8%; Pred. No. 2.2e-148; cive 31; Mismatches 25; Indels 0
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                    Last sequence update)
Last annotation update)
Created)
01-OCT-2000 (TrEMBLrel. 15, Create 01-OCT-2000 (TrEMBLrel. 15, Last 8 01-MR-2003 (TrEMBLrel. 23, Last 8 spinal cord-derived growth factor.
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Pfam, PF00431; PUB; 1.
SMART; SM0042; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
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NCBI_TaxID=9031;
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     LKEEVKLYSCTPRNFSVSIREELKRTDTIFWPGCLLVKRCGGNCACCLHNCNECQCVPRK 300
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MEDLINE=20417814; PubMed=10960785;
Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
The mouse Pdgfc gene: dynamic expression in embryonic tissues during
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Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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Last annotation update)
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wech. Dev. 96:209-213 (2000).
-! SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL, AF266725; AAF91483.1; -.
MGD; MGI: 1885631; PGdfc.
InterPro; IPR000659; CUB, domain.
InterPro; IPR000072; PD_Growth_factor.
Pfam; PR00431; CUB; 1.
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS01180; CUB; 1.
SROSITE; PS01180; CUB; 1.
SROSITE; PS01180; CUB; 1.
SROURCE 345 AA; 38886 MW; FA1486BED
                                                                                                                                                                                                                                                                                                                     01-007-2000 (TrEMBLrel. 15, Creat
01-007-2000 (TrEMBLrel. 15, Last
01-MAR-2003 (TrEMBLrel. 23, Last
platelet-derived growth factor C.
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                                                                         SEQUENCE FROM N.A.
PubMed=11331881;
  Wistow G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61 DLCKYDFVEVEEPSDGSVLGRWCGSGTVPGKQTSKGNHIRIRFVSDEYFPSEPGFCHYYS 120
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Liu Y.Q., Wang X.Y., Zhao B., Sheng H., Zhao X.W., Liu S.,
Xu Y.Y., Ye J., Song L., Gao Y., Zhang C.L., Zhang J., Wei Y.J.,
Cao H.Q., Zhao Y., Liu L.S., Ding J.F., Gao R.L., Wu Q.Y., Qiang B.Q.,
Yuan J.G., Liew C.C., Zhao M.S., Hui R.T.;
Submitted (DEC-1998) to the BMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    W.J. A.R. 2001 (T.EMBLrel. 16, Created) 01-MAR-2001 (T.EMBLrel. 16, Last sequence update) 01-MAR-2001 (T.EMBLrel. 16, Last sequence update) 8PINAL CORD-4 (T.EMBLrel. 23, Last annotation update) factor of form of form of factor long form (Platelet-derived growth factor 10 FGF OR PDGFD.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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STRAIN-Sprague-Dawley, TISSUE-Skin,
Brown S.A., Coberly D.M., Rohrich R.R., Chao J.J.;
"Platelet Derived Growth Factor C (PDGF-C) Expression in Wound
                                                                                                                                                                                                                                                                                                                                               Length 258;
                                                                                                                                                                                                                                                                                                                                                                                         12; Indels
                                                               258 258 AA; 29255 MW; 88625B989FCC3F8B CRC64;
                                                                                                                                                                                                                                                                                                                                               67.8%; Score 1260; DB 11;
85.6%; Pred. No. 3.9e-114;
iive 25; Mismatches 12;
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Matches 220; Conservative
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SEQUENCE
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A BEDLINE-121231380; PubMed-11331882;

A MEDLINE-21231380; PubMed-11331882;

A Gises N.A., Joffers M., McDonald W.F., Chillakuru R.A.,

Gises N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,

Gises N.A., Rothberg J.M., Lickenstein H.S.;

Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shimkets J.,

Shimkets R.A., Rothberg J.M., Lickenstein H.S.;

R. Nat. Call Blad. 3:517-521(2001).

1. - SIMILARITY: CONTAINS I CUB DOMAIN.

2. - InterPro; IPRO0051; FD_Growth_factor.

2. - InterPro; IPRO0051; TonB_DoxC.

3. Romain.

3. SWART; SWO041; CUB; 1.

3. SWART; SWO041 CUB; 1.

3. SWART; SWO041 CUB; 1.

3. SWART; SWO041 CUB; 1.
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                                                                                                                                             Bergsten B., Untela M., Li X., Pietras K., Ostman A., Heldin C.H., Alitalo K., Eriksson U.; Pietralo K., Eriksson U.; protease-activated ligand for the PDGF betareceptor.";
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39.9%; Score 741.5; DB 4; Length 370;
Best Local Similarity 43.6%; Pred. No. 1.6e-63;
Matches 159; Conservative 59; Mismatches 114; Indels 33;
"Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
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PROSITE; PS50278; PDGF. 2; 1.
PROSITE; PS0430; TONB DEPROBRY REC 1; 1.
SEQUENCE 370 AA; 42848 MW; D387F485E7BB7674 CRC64;
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STRAIN-BALB/C;
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       01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
11-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Iris-expressed growth factor short form (Spinal cord-derived growth factor-B).
                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                  Query Match

39.9%; Score 740.5; DB 4; Length 364;
Best Local Similarity 43.2%; Pred. No. 2e-63;
Matches 156; Conservative 61; Mismatches 113; Indels 31;
                                                                                                                                                                                                      Straubberg R.;
Straubberg R.;
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
Submitted (MAY-2002) to the EMBL/GenBank/DDBJ databases.
BMBL; AV027518; AAK20082.1; -.
InterPro; IPR000859; CUB domain.
InterPro; IPR000072; PD_Growth_factor.
InterPro; IPR000531; TonB_boxC.
Pfam; PF00431; CUB. 1.
                                                                                                                                                     "Iris-expressed Growth Factor (IEGF).";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
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PROSITE; PS0278; PDGF_2; 1.
PROSITE; PS00430; TONB_DEPENDENT_REC_1; 1.
SEQUENCE 364 AA; 42166 MW; 245C53E8DDBA9EAC CRC64;
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Last annotation update)
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01-DEC-2001 (TrEMBLrel. 19;
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Best Local Similarity
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Arakawa T., Azawa K., Akahira S., Akimura T., Arai A., Aono H.,
A Arakawa T., Bono H., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
A Hanagaki T., Hara A., Hayatsu N., Hiramokor K., Hirakaka T., Hori F.,
Imotani K., Ishii Y., Itoh M., Izawa M., Kasukawa T., Kato H.,
A Kawai J., Kojima Y., Konno H., Kouda M., Koya S., Kurihara C.,
A Matsuyama T., Miyazaki A., Nishi K., Nomura K., Numazaki R., Ohno M.,
A Okazaki Y., Okido T., Owa C., Salto H., Saito R., Sakai C., Sakai K.,
A Sano H., Sasaki D., Shibata K., Shibata Y., Shinagawa A., Shiraki T.,
A Sogabe Y., Suzuki H., Tagami M., Tagawa A., Takahashi F., Tanaka T.,
A Tajima Y., Toya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
A Tajima W., Hayashizaki Y.;
Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
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SECUENCE FROM N.A.
STRAIN=C57BL/G0; TISSUE=Body;
MEDLINE=C57BL/G0; TISSUE=Body;
MEDLINE=C57BL/G0; TISSUE=Body;
MEDLINE=C374; PubMed=11041159;
Konno H., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
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Konno H., Okazaki Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
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Konno H., Shibata K., Hayatsu N., Sugahara Y., Itoh M.,
Konno H., Shibata K., Hayatsu N., Shibata K., Itoh M.,
Konno H., Shibata K., Hayatsu N., Shibata K., Itoh M.,
Konno H., Shibata K., Hayatsu N., Shibata K., Itoh M.,
Konno H., Shibata K., Hayatsu N., Shibata K., Itoh M.,
Konno H., Shibata K., Hayatsu N., Hayatsu N., Shibata K., Itoh M.,
Konno H., Shibata K., Shibata K., Itoh M., Shibata K., Itoh M.,
Konno H., Shibata K., Shibata K., Itoh M., Shibata K., Itoh M.,
Konno H., Shibata K., Itoh M., Shibata K., Itoh M.,
Konno H., Shibata K., Itoh M., Shibata K., Itoh M.,
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Platelet-derived growth factor D (18-day embryo whole body cDNA, RIKEN full-length enriched library, clone:1110003109 product:platelet-derived growth factor D).
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MEDLINE=21231380; PubMed=11331882;
LaRochelle W.J., Jeffers M., McDonald W.F., Chillakuru R.A.,
Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet
Giese N.A., Lokker M.D., Deegler L.L., Rittman B., Shimkets J.,
Shimkets R.A., Rothberg J.M., Lichenstein H.S.;
"PDGF D, A Novel Protease-Activated Growth Factor.";
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Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=99279253; Pubmed=10349636;
Cardinci P., Hayashizaki Y.;
Cardinci P., Hayashizaki Y.;
Meth. Enzymol. 303:19-44(1999).
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STRAIN=C57BL/6J; TISSUE=Body;
MEDLINE=21085660; PubMed=11217851;
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MEDLINE=22354683; PubMed=12466851;
The PANTOM CONSORTIUM,
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                                                                                                                                                                                                                                                                                                                                 musculus (Mouse)
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SMART; SM00042; CUB; 1.
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16 QRRGTQAESNLSSKFQFSSNKEQNGVQD-PQHERIITVSTNGSIHSPRFPHTYPRNTVLV
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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MEDLINE=21092670; PubMed=11162582;
MEDLINE=21092670; PubMed=11162582;
MOIGCULAR Cloring of SCDGF-B, a Novel Growth Factor Homologous SCDGF/PDGF-C/fallotein.";
MOIGCULAR CLORING OF SCDGF-B, a Novel Growth Factor Homologous SCDGF/PDGF-C/fallotein.";
MOIGCULAR CLORING SCOMMUN. 280:733-737(2001).
-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
EMBL; AB052170; BAB18920.1;
InterPro; IPR000859; CUB domain.
InterPro; IPR000859; CUB domain.
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PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2003 (TrEMBLrel. 23, Last annotation update)
Spinal-cord derived growth factor-B.
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WRLVAVEENVWIQLTFDERFGLEDPEDDICKYDFVEVEEPSDGT--1LGRWCGSGTVPGK 132
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                                                                                                                                                                                                                                                                                                                                                                                 195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SVSIREELKRIDIIFWPGCLLVKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRP-- 313
                                                                                                                                                                                                                                                95
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                                                                                                                                                                                                                                                                                                                                                     96 LEDPEDDICKYDFVEVEEPSDGT--ILGRWCGSGTVPGKQISKGNQIRIRFVSDEYFPSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PGFCIHYNIV---MPQFTEAV------SPSVLPPSALPLDLLNNAITAFST
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                                                                                                                                                                                                                                             37 EQNGVQD-PQHERIITVSTNGSIHSPRPPHTYPRNTVLVWRLVAVBENVWIQLTFDERFG
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Wataryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ch 23.4%; Score 435.5; DB 11; Length 261; 1 Similarity 39.8%; Pred. No. 5.9e-34; 97; Conservative 45; Mismatches 73; Indels 29;
                                                                                                                                                                                           28;
                                                                                                                                      Length 370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Similar to platelet-derived growth factor, D polypeptide
                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Strausberg R.; 
submitted (UUN-2002) to the EMBL/GenBark/DDBJ databases. 
Submitted (UUN-2002) to the EMBL/GenBark/DDBJ databases. 
EMBL, BC030896; AAH30896.1; -. 
MGDI, MGT:12193035; PGGFG. 
InterPro; IPR000859; CUB_domain. 
Pfam; PF00431; CUB; 1. 
PROSITE; PG01180; CUB; 1. 
ERQUENCE 261 AA; 30228 MW; ZEEC3F6373A52D09 CRC64;
SMART; SM00141; PDGF; 1.
PROSITE; PS01180; CUB; 1.
PROSITE; PS50278; PDGF 2; 1.
SEQUENCE 370 AA; 42809 MW; 7BE8A251F679BF73 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
Last sequence update)
Last annotation update)
                                                                                                                                   39.6%; Score 736; DB 11;
45.6%; Pred. No. 5.6e-63;
iive 57; Mismatches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        314 -KTGVRGLHKSLTDVALEHHEECDCVC 339
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | : : | |: | || || || || 338 FKRRGKAKNMALVDIQLDHHERCDCIC 364
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002 (TrEMBLrel. 22, 01-OCT-2002 (TrEMBLrel. 22, 01-MAR-2003 (TrEMBLrel. 23,
                                                                                                                                                                                                Matches 149; Conservative
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Best Local Similarity
                                                                                                                                                                     Local Similarity
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157 KSPGFPEKYPNNLDCTFMIPAPKMSEIVLEPESFELEPDTQP~----PAGVFCRYDRL 209
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                                                                                                                                                           Q8AXP1
                                                                                                   RESULT 15
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                                    133 QISKGNQIRIRFVSDEYFPSEPGFCHYNIVMPQFTEAV-------SPS 174
                                                                                                                             175 VLPPSALPLDLLNNAITAFSTLEDLIRYLEPERWQLDLEDLYRPTWQLLGKAFVFGRKSR 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
Lee P., Goishi K., Davidson A., Mannix R., Zon L., Klagsbrun M.;
"Neuropilin-I is required for normal vascular development and is a mediator of VEGF-dependent angiogenesis in zebrafish.";
"Submitted (NOV-201) to the EMBL/GenBank/DBJ database."

Li Submitted (NOV-201) to The EMBL/GenBank/DBJ databases.
-!- SUBCELLUAR LOCATION: TYPE I MEMBRANE PROTEIN (BY SIMILARITY).
-!- SIMILARITY: CONTAINS I WAM DOWAINS.
-!- SIMILARITY: CONTAINS I WAM DOWAINS.
-!- SIMILARITY: CONTAINS I MAM DOWAIN.
-!- SIMILARITY: CONTAINS I FS/8 TYPE C DOWAIN.
-!- SIMILARITY: CONTAINS I FS/8 TYPE C DOWAIN.
-!- SIMILARITY: CONTAINS I FS/8 TYPE C DOWAIN.
-!- SIMILARITY: CONTAINS I MAM Gomain.
-- REMBL: PRO00998; MAM Gomain.
-- REPERSON PRO00998; MAM Gomain.
-- REPROSON PRO00998; MAM Gomain.
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-- REPROSON PROFOSSY: FS/8 TYPE C DOWAINS.
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-- REPROSON PROFOSSY: MAM: I.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Brachydanio rerio (Zebrafish) (Danio rerio).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Meopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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SEQUENCE 923 AA; 102492 MW; 2ED84B129AA92B2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8QEX6,
01-JUN-2002 (TrEMBLrel. 21, Created)
01-JJN-2002 (TrEMBLrel. 21, Last sequence update)
01-FAR-2003 (TrEMBLrel. 23, Last annotation update)
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SMART; SM0221; FASC; 2.
SMART; SM0221; FASC; 2.
SMART; SM0137; MAM; 1.
PROSITE; PS01180; CUB; 2.
PROSITE; PS01285; FAS8C_1; 1.
PROSITE; PS01286; FAS8C_2; 2.
PROSITE; PS00740; MAM 1.
PROSITE; PS50060; MAM 2; 1.
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44 VSYYPSQKCIWVITAPGPNQRILINFNPHFDLEDRE---CKYDYVBVBGVDENQLVGK 100
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                                                                                                                                                                                                                                     Enachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Shôji W., Tawarayama H.;
"The cloning and expression of neuropilin-1.";
Submitted (UTL-2002) to the EMBL/GenBank/DDBJ databases.
EMBL, ABO87775; BACS3657.1; -.
SEQUENCE 923 AA; 102541 MW; 0E6CE33ED28A21F7 CRC64;
                                                              01-MAR-2003 (TrEMBLrel. 23, Created)
01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
923 AA
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PRELIMINARY;
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November 25, 2003, 22:28:25; Search time 3795.28 Seconds (without alignments) 16556.656 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries
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score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	AR210624 Sequence AR232022 Sequence AR247650 Sequence AX391260 Sequence AX391260 Sequence AX2944913 Homo sapi AX234498 Sequence AX03434 Homo sapi AX739931 Sequence AR282949 Sequence AR282949 Sequence AX11878 Sequence AX11878 Sequence AX11878 Sequence AX11878 Sequence AX11878 Sequence AX11878 Sequence AX11878 Sequence AX11878 Sequence AX11873 Sequence AX11873 Sequence AX11873 Sequence AX11873 Sequence	Seque Seque Seque Seque Seque Mus Mus Mus Mus Mus	AR282950 Homo sapl AR282950 Sequence AX119274 Sequence AX273960 Sequence AX027962 Sequence AX027962 Sequence AX027963 Sequence AX027982 Sequence AX027983 Sequence AX027993 Sequence AX027968 Sequence AX027968 Sequence AX027968 Sequence AX027968 Sequence AX027968 Sequence AX027968 Sequence AX027968 Sequence AX027968 Sequence AX027968 Sequence	TS DNA linear PAT 20-JUN-2002
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FEATURES Location/Qualifiers source 1.2825 BASE COUNT 849 a 522 c 605 g 848 t 1 others ORIGIN Query Match 99.8%; Score 1532.6; DB 6; Length 2825;	Best Local Similarity 99.3%; Fred. No. 0; Indels 0; Gaps 0; Matches 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0; Qy GTAAHTCCAGTHCAACAACAACAACAACAACAACAACAACAACAACAACAA	64 64 401	124 CAA 461 CAA	Qy 184 TTACGTTTGATGAAAGTTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGAT 243

IGTACTACAAACCTGGTTTTTAAAAGGAACTATGTTGCTAGAAT 1503 ACTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGG 1383 linear PAT 20-DEC-2002 ö TCTTGCCCAGAGCTGTGCAGTGCAGTGGTGATTCTATTAGAGAA 1023 CATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1083 1480 AGATCACCAGCTAGTTTCAGAGTTACCATGTACGATATTCCACTAGC 1263 CTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT 1143 TICTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 123 coding vascular endothelial cell growth factor-E 0; Gaps .8%; Score 1532.6; DB 6; Length 2825; 0.9%; Pred. No. 0; e 1; Mismatches 0; Indels 0; 1 others SCTGATAGGACAGACTGGA 1536 DNA u 183-A 1 24-SEP-2002; nn/Qualifiers 15 848 2825 bp patent US 6455283. sm="unknown" c 605 g uo, S.S. 7273902

Oy 1324 CTGTGCAAGTGAGCACCTC Db 1687 CTGTGCAAGTGAGCACCTC OY 1384 CCTAAAATCGTATAAAATC OY 1747 CCTAAAATCGTATAAAATC OY 1444 ACCAGAACATTCTATGTA OY 1504 TAAACTTGTGTATAAATC Db 1807 ACCAGAACATTCTATGTA Db 1807 ACCAGAACATTCTATGTA	RESULT 4 AX391260 LOCUS LOCUS DEFINITION Sequence 3 from Pater ACCESSION AX391260. VERSION AX391260.1 GI:19699: KEYWORDS SOURCE Homo sapiens (human) ORGANISM Homo sapiens Eukaryota; Metazoa; Mammalia; Eutheria; REFREENCE IEMEMBERS; Perrara, N. Williams	Godowski, P.J., Gurne Pitti, R.M., Wood, W.I. Watanabe, C.K. TITLE Promotion or inhibit JOURNAL Patent: WO 0073445-A Genetech Inc. (US) FRATURES Location/Qu SOURCE // Crganism="// Mol_type="// Mol_typ	ORIGIN ORIGIN ORIGIN ORIGIN Dest Local Similarity 99.3%; Matches 1532; Conservative OY 4 GTAAATTCCAGTTTTCCA	427 124 124 487	Oy 184 TTACGTTGAAGAN Db 547 TTACGTTTGATGAAGAN Qy 244 TTGTAGAAGTTGAGGAAC Qy 244 TTGTAGAAGTTGAGGAAC COY 304 CTGTAGAAGTTGAGGAAC Oy 304 CTGTACCAGGAAAACAG Db 667 CTGTACCAGGAAAACAG Oy 364 AATATTTCCTTCTGAAC
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ö TGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGG 1383 486 linear PAT 23-MAR-2002 ATTIGGGCTIGAAGACCCAGAAGATGACATATGCAAGTATGATT 243 123 ACCCAGTGATGGAACTATTAGGGCGCTGGTGTGGTTCTGGTA 303 ACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 423 is,P.M., Baker,K.P., Ashkenazi,A.J., Goddard,A., ley,A.L., Kuo,S.S., Mark,M.R., Marsters,S.A., I., Gerber,H., Gerritsen,M.E., Paoni,N.F. and tion of angiogenesis and cardiovascularization. A 3 07-DEC-2000; Chordata, Craniata, Vertebrata, Buteleostomi; Primates, Catarrhini, Hominidae, Homo. TACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC ACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC PAGCAACAAGGAACAGAACAGATACAAGATCCTCAGCATGAGA ICTGGATTTTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 0; Gaps DB 6; Length 2849; 1 others 0; Indels DNA 850 t b; Score 1532.6;
k; Pred. No. 0;
1; Mismatches ="Homo sapiens" ="genomic DNA" "taxon:9606" 619 g 850 2849 bp ent WO0073445. ualifiers 9933

RESULT 6 AF244813

ALAGQRRGTQAESNLSSKFQFSSNKEQNGVQDP NTVLVWRLVAVEENVWIQLTPDERFGLEDPEDD TVPGKQISKGNQIRIRFVSDEYPEREPGFCHY LNNATTAFSTLEDLIRYLEPERWQLDLEDLYRP BYRLYSCTPRNFSVSIREELKRTDTIFWPGCLL TKKYHEVLQLRPKTGVRGLHKSLTDVALEHHEE ö NA linear PRI 27-AUG-2001 factor C mRNA, complete cds. CAGCCCAAGGTTCCTCATACTTATC 123 AGTACAGCAAAATGTATCCATACAAC 183 st for platelet-derived growth Ralpha) "E e PDGF/VEG growth factor CUB domain and the C-terminal AGAAGATGACATATGCAAGTATGATT 243 GGGAGTACAAGATCCTCAGCATGAGA 63 a, Vertebrata; Buteleostomi; nini; Hominidae; Homo. L., Abramsson,A., Uutela,M., T., Li,H., Soriano,P., K., Ostman,A. and Eriksson,U. igand for the PDGF 0; Gaps ute for Cancer Research, 3-171 77, Sweden DB 9; Length 2152; growth factor C" 0; Indels 1 others 유 전

OY 1384 CCTAAAATCGTATAAAATC DD 1651	RESULT 7 AZ24498 LOCUS LOCUS DEFINITION Sequence 148 from Pa ACCESSION AX234498.1 GI:15593 KEYWORDS COURCE CORGANISM Homo sapiens CORGANISM ENkaryota; Metazoa; Mammalia; Eutheria;	AUTHORS Alitalo, K.M. and Jel TITLE Materials and method factor dnas and prot JOURNAL PATENT: WO 0162942-A LUDWIG INSTITUTE FOR FEATURES I cation/Qu source I .3007	/mol_type=" /db_xref="to- /db_xref="to- /note="unna /codon_stax /protein_id /protein_id /translarie	QHERIITVSTR ICKYDFVBVBE NIUMPQFTBAV TWOLLGKAPVB VKRCGGNCACC CDCVCRGSTG BASE COUNT 858 a 613 c ORIGIN	Query Match Best Local Similarity 99.9% Matches 1531; Conservative Qy 4 GTAAATTCCAGTTTTCCA	4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	Oy 124 CAAGAAATACGGTCTTGC Db 694 CAAGAAATACGGTCTTGC OY 184 TTACGTTTGATGAAAGAC Db 754 TTACGTTTGATGAAAGAC	Oy 244 TIGIAGAAGITGAGGAA
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ods involving hybrid vascular endothelial growth
veins and screening methods for modulators
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R. Chromer RESEARCH (US) ; Licentia OY (FI) TACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 123 ATTIGGGCTIGAAGACCCAGAAGAIGACAIAIGCAAGIAIGAIT 243 ACCCAGTGATGGAACTATATTAGGGCGCTGGTGTGGTTCTGGTA 303 LAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA 63 Chordata, Craniata, Vertebrata, Euteleostomi, Primates, Catarrhini, Hominidae, Homo. 0; Gaps Score 1531; DB 6; Length 3007; Pred. No. 0; 1, Indels linear GATAGGACAGACTGGA 1536 named protein product" DNA 1; Mismatches 3007 bp 1 Patent WO0162942. ="Homo sapiens" ="genomic DNA" "taxon:9606" 901 ld="CAC69781.1" GI:15593482" 635 g 3481 ۰۰ ۰۰ مدر مدر

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VKRCGGNCACCLHNCNECQCVPSKVTKKYHEVLQLRPRTGVRGLHKSLTDVALEHHEE
CDCVCRGSTGG"
2974. .2979
CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 1443
                                                  2014 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 2073
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Teal, Y.J., Lee, R.K., Lin, S.P. and Chen, Y.H.
Identification of a novel platelet-derived growth factor-like gene, fallotein, in the human reproductive tract
Biochim. Biophys. Acta 1492 (1), 196-202 (2000)
                                                                                                                                                                                                                                  1444 ACCAGAACATICTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
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Statisty. Lace, R.K.K. and Lin, S.P.
Diract Submission
Submitted (14-SEP-1998) Dept. Medical Research, Mackay Memorial
Hospital, 45 Min Sheng Road, Tamshui, Taipei County 25115, Taiwan
1. 1003007
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Complete cds.
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1 (bases 1 to 1804)

3 (libertson), D.G., Duff, M.E., West, J.W., Kelly, J.D., Sheppard, P.O., Hofstrand, P.D., Gao, Z., Sheemaker, K., Bukowski, T.R., Moore, M., Feldhaus, A.L., Humes, J.M., Palmer, T.E. and Hart, C.E. that binds to PDGF alpha and beta receptor

J. Biol. Chem. 276 (29), 27406-27414 (2001)
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Inc., 1201 Eastlake Avenue Bast, Seattle, WA 98102, USA
CCTAAAATCGTATAAAATCTGGA-TTTTTTTTTTTTTTGCTCATATTCACATATGTA
                             AACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAA
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Gao, Z., Hart, C., Piddington, C., Sheppard, P., Shoemaker, K.,
Gilbertson, D., West, J. and O'Hara, P.J.
Direct Submission
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	RESULT 12 AZ282949 LOCUS AR282949 LOCUS DEFINITION Sequence 1 from patent US 6528050. ACCESSION AR282949 VERSION AR282949.1 GI:29719770 KEYWORDS SOURCE Unknown. ORGANISM Unknown. ORGANISM Unknown. ORGANISM Unknown. TITLE Gao,Z., Hart,C.E., Piddington,C.S., Sheppard,P.O., Shoemaker,K.E., Gilbertson,D.G. and West,J.W. TITLE Growth factor homolog zvegf. JOURNAL EAATURES LOCATIONALIFIERS 1.1760 BASE COUNT 494 a 373 c 411 g 482 t	tch 15.22; Conservative 1 Similarity 99.8%; Fred. No. 0; 15.22; Conservative 1 Mismatches 4 GTAAATTCCAGTTTTCCAGCAACAGGAACAGA 64 GAATTTCCAGTTTTCCAGCAACAGGAACAGAACAGA 64 GAATTTTTACTGGTCTTACTATGGAACTATC 124 CAAGAATACGGTCTTACTATGGAACTATCAGAACAGAAC
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ACCESSION AX044518 VERSION KEYWORDS Homo sapiens BURATYCLE AN Metazoa, Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. AUTHORS Gilbert, T., Hart, C.E., Sheppard, P.O. and Gilbertson, D.G. Growth factor homolog vegf4 JOURNAL Patent: WO 0066736-A 32 09-NOV-2000; PEATURES JOURNAL PATENTIE JAMOGENETICS, Inc. (US) PEATURES 1. 176 ACTARIAN HOMO SAPIENS 1. 176 ACTARIAN HOMO SAPIENS CDS 1. 176 ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENS ACTARIAN HOMO SAPIENT ADDRESSIVERENCE AND AND SAPIENT HOMO SAPIENT AND ARTERIAN HOMO SAPIENT	Query Match 98.4%; Score 1511; DB 6; Length 1760; Best Local Similarity 99.8%; Pred. No. 0; 1; Indels 1; Gaps 1; Qy 4 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGAGTACAAGATCCTCAGCATGAGA 295 Qy 64 GAATTATTACCAGTTTTCCAGCAACAAGAACAACGAGGAGTACAAGATCCTCAGCATGAGA 295 Qy 64 GAATTATTACCAGTTTTCCAGCAACAACAGAACAGACCAAGATTCCTCAGCATGAGA 295 Qy 64 GAATTATTACCTGTTTACTACTAATGAACATTACAACCCCAAGGTTTCCTCATACTTATC 355 Qy 124 CAAGAAATACCGTTTGGTATGAGATTAGTAGCAGTACAAGATTACATACTTATC 355 Qy 124 CAAGAAATACCGTTTGGTATGGAGTTTAGTAGCAGTAGAGAAATGTATGATACAAC 415 Db 356 CAAGAAATACGGTCTTGGTATGGAGTTTAGTAGCAGTAGAGAAATGTATGATGATTACAACTAGATGATACAATTGCAAGTTTGATGATTATAGGAGCAGTAGAAATGCAAGTTGAAGATTGAAGATTGTAATCTAGAAGTTCTGATGAAGATTGTAATCTAGAAGTTCTGATGAAGAATTGTAATCTAGAAATTGTAATCTGATGAAGATTTGTAATCTGATGAAATTGTAATCTGATTCTGATGAAGAATTGTAATCTGAATCTAATACAAATTGTAATCTGAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAATACAAATTGTAATCTAAAATTCAAAATTGTAATCTAAATTAAATTCAAAATTGTAATCTAAATTAAATTAAATTAAAATTGTAATCTAAAATTAAAATTAAAAATTGTAATCTAAAATTAAAATTAAAAATTGTAATCTAAAATTAAAAAAAA	
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AX118785.1 GI:14035734 Homo sapiens (human) SM Homo sapiens sapiens asplems asplems but averaged asplems but averaged by the sapiens but averaged by the sapiens but averaged	Query Match 98.8; Scote 15.1; DB 6; Length 1/60; Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps 4 GTABATTCCAGTTTTCCAGCAACAAGGAACAGAACGAGATACCAGATCCTCAGCATGAGA 63	236 GTAAATTCCAGTTTTCCAGCAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA 64 GAATTATTACTGTGTCTACTAAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATC	QY 124 CAAGAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGTATGGATACAAC 183	QY 244 TIGTAGAAGITGAACCCAGIGATGGAACTATATAGGGGGCTGGTGTGGTTCTGGTA 303 Db 476 TIGTAGAAGITGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGGTTCTGGTA 535	OY 304 CIGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363	QY 364 AATAITITCCTICIGAACCAGGGTTCTGCACTACAACAITGTCATGCCACAATTCA 423	OY 424 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483	OY 484 AIGCTAIDACTGCCTTTAGTACCTTGGAAGACCTTATTCGAIDTCTTGAACCAGAGAGI 543
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AB033831 1817 bp mRNA linear PRI 26-JUL-2000 Homo sapiens hSCDGF mRNA for spinal cord-derived growth factor, complete cds. AB033881

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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Hamada, T., Ui-Tel, K. and Miyata, Y.
Hamada, T., Ui-Tel, K. and Miyata, Y.
Direct Submissorion
Submitted (25-00T-1999) Tsuyoshi Hamada, Nippon Medical School,
Department of Pharmacology; 1-1-5, Sendagi, Bunkyo-ku, Tokyo
113-8602, Japan (E-mail: thamadd@nms.ac.jp,
Tel:81-3-3822-2131 (ex.5277), Fax:81-3-5814-1684)
Location/Qualifiers
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A novel gene derived from developing an unique member of the PDGF/VEGF family lett. 475 (2), 97-102 (2000)
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/db_xref="taxon:9606"
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Copyright (c) 1993 - 2003 Compugen Ltd.
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Listing first 45 summaries
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1536
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	CDNA encoding a fr Human VEGF-E DNA. DNA encoding human Human PRO200 nucle Human PRO200 (UNQ1 Human PRO200 (VEGF Human PRO200 prote Human PRO713 cDNA
SUMMARIES	AAA12524 AA223691 ABS57294 AAZ34296 AAA88515 AAC86579 AAA7621
DB	2222222
* Query Match Length DB	28849 28849 28849 28849 28849 28849 28849
% Query Match	000000000000000000000000000000000000000
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Result	

Human cDNA sequenc	Human PRO200 CDNA.	Human PRO200 codin	Human angiogenesis	cDNA encoding huma	Human cDNA encodin	DNA encoding novel	cDNA encoding huma	cDNA encoding plat	Human RACE generat	Human TANGO 128 co	Bone morphogenic p	DNA encoding for h	cDNA encoding huma			×	Human LP8, a PDGF-	Human platelet-der	DNA encoding human			Human Zvegf3 DNA.	Human cDNA encodin	Human zvegf3 codin	DNA encoding human		Bone morphogenic p	Human VEGF/PDGF-li	VEGF/P	Human VEGF-X DNA i	Human VEGF-X DNA f	1	MBP-ZVEGF3 fusion	Human zvegf 3/malt	DNA encoding human	Human VEGF-X DNA f
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ALIGNMENTS

ВÞ.

AAA12524 standard; cDNA; 1536

RESULT 1

AAA12524

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Platelet-derived growth factor C; PDGF-C; cell proliferation; growth factor; heparin; connective tissue; wound healing; VEGF-F; fibroblast mitogenesis; PDGF alpha receptor activation; tumour growth; choriocarcinoma; Wilms tumour; megakaryoblastic leukaemia; lung carcinoma; erythroleukemia; tissue remodelling; ss.
                                                           cDNA encoding a fragment of platelet-derived growth factor C (PDGF-C).
                                                                                                                                                                                               3..959
/*tag= a
/product= "platelet-derived growth factor C fragment"
/transl_except= (pos: 861..863, aa: Lys)
                                                                                                                                                                                    Location/Qualifiers
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                                    25-JUL-2000 (first entry)
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            AAA12524;
                                                                                                                                                             Homo
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The present sequence encodes a human platelet-derived growth factor C (PDGF-C) (formally designated VBGF-F) fragment. PDGF-C polypeptides have the ability to stimulate and enhance proliferation or differentiation, and/or growth or motility of cells expressing a PDGF-C receptor.

and/or growth or motility of cells expressing a PDGF-C receptor.

PDGF-C polypeptides can be used in pharmaceuticals for promoting cell proliferation, preferably in combination with one other growth factor and heparin. Pharmaceuticals compressing PDGF-C polypeptides can also be used for stimulating connective tissue or wound healing. The PDGF-C polypeptide can be enzymatically processed to generate the active truncated form of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and used to regulate the receptor-binding specificity of PDGF-C and used to induce PDGF used to promote fibroblast connected form of unduce PDGF used to induce PDGF at unduring inventy, megakaryoblastic contraction.

PDGF-C antagonists can be used to inhibit tumour growth of a tumour correction, will be used to inhibit tissue of pDGF-C. PDGF-C antagonists can also be used to inhibit tissue carcinoma and erythroleukemia, can be identified by testing for expression of remodelling during linvasion of tumour cells into a normal population of cells. Antagonists can also be used to treat fibrotic conditions, cells into a normal population of especially found in the lung, kidney or liver.
                                                                                                                                                                                                                                                                                                                            Novel DNA encoding PDGF-C useful to stimulate or enhance proliferation, differentiation, growth and motility of cells expressing the PDGF-C
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Betsholz C;
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UNIV HELSINKI LICENSING LTD
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98US-0110749.
98US-0113002.
98US-0113002.
99US-0135426.
99US-0144022.
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Heldin C,
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P-PSDB; AAY84558.
  12-NOV-1998;
03-DEC-1998;
18-DEC-1998;
21-MAY-1999;
15-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention describes the isolation of a novel human vascular endothelial cell growth factor-E (VEGF-E) polypeptide which has endothelial cell growth factor-E (VEGF-E) polypeptide which has cranged to tranquillizer, vulnery and cardiant activity. VEGF-E can be administered therapeutically, especially by expressing encoding polynucleotides, to treat cardiovascular or endothelial disorders in mammals, especially commanders in wammals, especially commanders in wammals, especially commanders in mammals, especially commanders in mammals, especially can be combined with a carrier in pharmaceutical compositions, which can be administered to treat disorders as above. VEGF-E can be used to creat angiogenic disorders in mammals (especially humans) e.g. cancer or serelated macular degeneration. It can be used to generate antibodies, useful therapeutically as antagonists, as above. The antibodies are also useful therapeutically as antagonists, as above. The antibodies are also useful to detect VEGF-E polypeptide, especially to diagnose cardiovascular, endothelial or angiogenic disorders in mammals (e.g. vascular disease, or neovascularization associated with tumor formation, by contacting the antibody with a tissue sample and detecting formation of an antibody-VEGF-E polypeptide complex. Polynucleotides encoding VEGF-E can be used to diagnose cardiovascular and endothelial disorders in mammals, by detecting abnormally high or low VEGF-E can be used to diagnose cardiovascular and endothelial endothelial customs in mammals, by detecting abnormally high or low VEGF-E gene expression in the susceptibility to a disease related to a mutated form of VEGF-E or
  1441 TAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATG 1500
                                                                                                                                                                                                                                                                                                                                                                                                                                                         VEGF-E; human; vascular endothelial cell growth factor; wound repair;
treatment; cardiovascular disorder; endothelial disorder; therapy;
tissue generation; regeneration; cardiac hypertrophy; cancer; detection;
angiogenic disorder; age-related macular degeneration; vascular disease;
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                                                                                AATTAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
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/product= "VEGF-E"
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cardiovascular, endothelial or angiogenic disorder such as a tumor), by detecting a mittation in the VEGF-E-encoding sequence isolated from a sample. They may also be used to produce probes useful to detect relater sequences or for gene mapping. This sequence encodes the human VEGF-E
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                                                                                                                                     Sequence 2825 BP; 849 A; 522 C; 605 G; 848 T; 1 other;
                                                                                                                                                                                 DB 20;
                                                                                      protein described in the method of the invention.
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                                                                                                                                                                               Score 1532.6;
Pred. No. 0;
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                                                                                                                                                                                                                           Matches 1532; Conservative
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                                                                                                                                                                                                           New nucleic acid encoding endothelial cell growth factor-E polypeptide, useful for diagnosing or treating a cardiovascular, endothelial or angiogenic disorder such as cancer, diabetes mellitus or atherosclerosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                        The present invention relates to the isolation of human vascular endothelial cell growth factors. B (VBGF-B, also referred to as PRO:200), and the polywucleotide sequence encoding it. VBGF-E is related to VBGF and bone morphogenetic protein I. VBGF-E is useful in wound repgir, as well as in the generation and regeneration of trissue. The sequences of the invention are useful for diagnosing or treating cardiovascular, endothelial or angiogenic disorders such as cancer, diabbetes mellitus, cardiac hypertrophy and atherosclerosis. The polymucleotide encoding VBGF-E is useful in the gene therapy of such disorders. The present sequence encodes human VBGF-E.
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                                                                                                                                                                                                                                                                                                                     Claim 2; Fig 1; 46pp; English.
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                    98US-0040220.
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                                                                            (GETH ) GENENTECH INC
                                                                                                                                                         WPI; 2003-066231/06.
P-PSDB; ABG72132.
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CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGGAGCACAGGAGGATAGCCGC
                                                                              TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAA
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Human, PRO; EST; expressed sequence tag; PCR primer; hybridisation; probe; blood coagulation disorder; cancer; cellular adhesion disorder; secreted protein; transmembrane protein; ss.
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   487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC 546
                                                                                                       CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG
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                                                                                      TIGIAGAAGTIGAAGGAACCCAGIGAIGGAACTAIATIAAGGGCGCIGGIGIGGTICTGGIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention describes secreted and transmembrane polypeptides and their polynucleotides. The nucleotide sequences are useful as sources of probes, primers, for chromosome mapping, and for generation of antisense sequences. They can also be used to create transgenic animals. The proteins can be used to treat a variety of diseases and disorders, depending on their function. Diseases that may be treated include blood coagularion disorders, cancers and cellular adhesion disorders. They may also be used to raise antibodies. AAZ33391 to AAZ34338, and AAY41685 to AAY41774 represent polymucleotide and polypeptide sequence given in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  64 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New secreted and transmembrane polypeptides and their polynucleotides, useful for treating blood coagulation disorders, cancers and cellular adhesion disorders -
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Pred. No. 0;
1; Mismatches
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9805-0085697.
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9805-0085704.
9805-008673392.
98US-0084366.
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P-PSDB; AAY41766.
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AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 786
                                                                                      AAC78458 to AAC78599 represent polynucleotide and EST (expressed sequence tag) sequences which encode secreted or transmembrane PRO polynecleotides and polypeptides have cytostatic activity. The PRO polynucleotides and polypeptides can be used for detecting the presence of PRO polypeptides in samples, for linking bioactive molecules to cells and for modulating biological activities of cells, using the polypeptides for specific targeting. The polypeptide targeting can be used to kill the target cells, e.g. for the treatment of cancers. The polypeptide pairs provide specific targeting of bioactive molecules to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CCATTITICIGGCCAGGIIGICICCCIGGIIAAACGCIGIGGGGGAACTGIGCCIGIIGIC 783
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Novel PRO polypeptides and polynucleotides used in detection methods, to target bloactive molecules to specific cells, and to modulate cellular activities -
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                                                                                                                                                                                                                                               the isolation of the PRO polynucleotide sequences.
                                                                                                                                                                                                                                                                                                    Score 1532.6;
Pred. No. 0;
1; Mismatches
                                                               Claim 2; Fig 206; 636pp; English
                                                                                                                                                                                                                                                                                                      99.8%;
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                                                                           CTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGG
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E, Fong S, Gao W, Gerber H, Gerritsen ME;
PJ, Grimaldi CJ, Gurney AL, Hillan KJ;
Napier MA, Pan J, Paoni NF, Roy MA;
TA, Tumas D, Williams PM, Wood WI;
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2000WO-US00277.
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Filvaroff E,
Godowski PJ,
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Goddard A, G
Kljavin IJ,
Shelton DL,
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           Homo sapiens.
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                                                         sig_peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present sequence is that of CDNA clone DNA29101-1272 or UNQ174 (ATC 20953) isolated from a human glioma cell line G61 CDNA (ATC 20953) isolated from a human glioma cell line G61 CDNA (ATC 20953) isolated from a human glioma cell line G61 CDNA (as delay, using probes (see AAA88523-36) based on an expressed sequence tag (see AAA88522) identified on the basis of homology to vascular endothelial growth factor (VEGF). The clone contains a single open creading frame encoding a 345-amino acid protein (see AAB39578) designated PRO200 or VEGF-E. The isolated CDNA can be used in the recombinant production of PRO200 (VEGF-E). The invention relates to the use of FRO polypeptides, including PRO200, to delay, prevent or rescue retinal cells such as retinal neurons selected from photoreceptors, retinal ganglion cells, displaced retinal ganglion cells, displaced retinal and photoreceptors, and supportive cells (including Mueller cells and pigment epithelial cells) from injury and degradation. The retinal cells are preferably photoreceptors and photoreceptor cell injury or death is caused by retinal injury, light or environmental trauma or by an ocular disease selected from retinitis pigmentosa, macular cears, retinal age-related, retinal degenerative myopia, acute retinal necrosis syndrome, traumatic chorioretinopathies or contusion such as Purtscher's retinapathy, contustion such as central or branch retinal vision occlusion, collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases, thrombocytopenic purpura, and collagen vascular diseases,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
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Kuo SS, La Fleur M,
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Matches 1532; Conservative
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1204 ATGITGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACTCACTAGC 1263 1567 ATGITGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTCATTCCACTAGC 1626 1567 ATGITGTATTTAAATAGATCACCAGCTAGTTTCAGTTACCATTCCACTAGCC 1626 1264 TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTAAGGTAATGTCAGTACAGGAAAAAA 1323 1627 TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGGAAAAAA 1686 1524 TGGGTACTGTATTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGGAAAAAA 1686 1525 TGGGTAGTGAGCACCTGATTCTGATAGGGTAATGTCAGTACAGGAAAAAA 1686 1526 TGGGTAGTGAGACCTGATTCCGTTGCCTTAAGGTCATAGTCAGGAAAAAA 1686 1527 TGGGTAGTGAGACCTGATTCCGTTGCCTTAAAGCTCCATGTCCTGGG 1746 1528 TGTGCAAAATCGTATAAAATCTGGTTAAATTTTTTTTTT	AACS8579 AACS8579 AACS8579 AACS8579; AACS8579; AACS8579; AACS8579; Buman PRO200 protein UN0174 encoding CDNA SEQ ID NO:1. Buman PRO200 protein UN0174 encoding CDNA SEQ ID NO:1. WHE Human; immune related disease; diagnosis; antiinflammatory; cardiant; which are mistanemic; immune related disease; diagnosis; antiinflammatory; cardiant; which are mistanemic; antiinflammatory; neuroprotective; which are mistanemic; antiinflammatory; neuroprotective; which are mistanemic; antiinflammatory antidabetic; neuroprotective; which are mistanemic; antiinflammatory mayopathy; systemic aclerosis; sarcticips; which are mistanemic; antidabetic; manual collection; which are mistanemic; and are according antidabetic; antipoportic; antidabetic; an
124 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAAAATGTATGGATACAAC 183 487 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAAATGTATGGATACAC 546 184 TTACGTTTGATGAAGATTTGGGCTTCAAGACCCAGAAGATGACATATGCATAGAT 243 547 TTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCATAGATT 606 248 TTGTAGAAGATTGAGGAACCCAGTGATGACCCAGAAGATGACATATGCATTGATT 606 241 TTGTAGAAGATTGAGGAACCCAGTGATGAACTATATTAGGGCGCTGGTGTGGTTCTGGTA 666 304 TTGTAGAAGATTGAGGAACCCAGTGATGAACTATATTAGGGCGCTGGTGTGGTTCTGGTA 666 305 TTGTAGCAGAAAACAGATTCTAAAGGAACCAAATTAGGATTAGTATTTGTATCTGATG 726 306 CTGTACCAGGAAAACAGATTCTAAAGGAAATAAAATTAGGATTAGTATTTGTATCTGATG 726 307 TTGTACCAGGAAACCAGTTTCTAAAGGAAATAAAATTAGGATTAGTATTTGTATCTGATG 726 308 AATATTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTATTCA 423 11	494 ATCCHTARCTCCTTTAGATACCTGGAAGACCTTATTCGATCCGAAGACATTGGAAGACTTCTTGACCAGAGACATTGGAAGACTTCTAGACCAGAGACATTGGAAGACTTCTAGACCAGAGACTTTGGAAGACTTTGGAAGACTTTGGAAGACTTTGGAAGACTTTTGAACCAGACTTTTGGAAGAAAATCCAGAGCTTTTGGAACAATTGCACACTTGAACCAATTGCAACTTCTTGAACAAGACTTTTTTGGAAGAAAATCCAGAGTGTTGATCTGAACCAATTGCAACTTCTTAGACAAGACTTATTTTGGAAGAAAATCCAGAGTGTTGATCTGAACCAATTGCAACTTCTTAACAAGAAAATTATTTGTAAAAAAAA

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1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 1086
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  <u>CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGGAAAAATGTATGGATACAAC</u>
                                                 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention describes sixty four human PRO proteins which can be used in the treatment of immune related diseases. The human PRO proteins, anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PRO anti-PR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sixty four PRO polypeptides, useful in the diagnosis and treatment of immune related disorders, e.g. systemic lupus erythematosis, rheumatoid arthritis, osteoarthritis, thyroiditis and diabetes mellitus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       KP, Goddard A, Gurney AL, Hebert C, Henzel W;
Pan J, Pennica D, Shelton DL, Smith V;
, Watanabe CK, Wood WI, Yan M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATAGAGA
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20-DEC-1999; 99W0-US30999.
30-DEC-1999; 99W0-US31274.
05-JAN-2000; 2000W0-US00219.
06-JAN-2000; 2000W0-US00277.
06-JAN-2000; 2000W0-US00377.
99WO-US21090.
99WO-US21090.
99WO-US21547.
99WO-US23089.
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18-FEB-2000; 2000WO-US04342.
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99WO-US28214
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99WO-US28409
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Kabakoff RC, Lu Y, Pan
Stewart TA, Tumas D, Wa
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P-PSDB; AAB33414.
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01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
02-DEC-1999;
                                                                              05-OCT-1999;
29-OCT-1999;
29-NOV-1999;
13-SEP-1999;
15-SEP-1999;
15-SEP-1999;
                                                                                                                                                                30-NOV-1999
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TTTTTGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 1026
                                                                                                                          The present invention describes nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovacular, endothelial or analysemic disorder in mammals by modulating cell proliferation, angiogenesis and cardiovacularisation, and for identifying agonists and antagonists of these processes. The nucleic acids and the proteins they encode may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PRO expression such as cardiovacular, endothelial or angiogenic disorders in mammals (e.g. atherosclerosis, cancers and cardiac hypertrophy). For example, the nucleic acids (NCS) and vectors associated with decreased PRO expression. AAA77510 to AAA77721 and AAB24388 to AAB2438 to AAB24435 repersent nucleotide and protein sequences used in
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                                        Nucleic acids encoding PRO polypeptides useful for preventing, diagnosing and treating diagnosing a cardiovascular, endothelial or angiogenic disorders in mammals -
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                                                                                                                                                                                                                                                                                                                       the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 0;
1; Mismatches
                                                                                                  Claim 61; Fig 49; 315pp; English
                                                                                                                                                                                                                                                                                                                                                                                99.8%;
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Best Local Similarity 99.9
Matches 1532; Conservative
 2000-412154/35.
             P-PSDB; AAB24412
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Kuo SS, Paoni NF, Smith V;
                  ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC
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Klein RD, F
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Williams PM, V
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Human secretory and transmembrane; PRO; mammalian; cancer; lung;

encoding for PRO200 polypeptide.

Human cDNA sequence

(first entry)

24-OCT-2001

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AAS21386;

BP

AAS21386 standard; cDNA; 2849

breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha; cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle; adipocyte; A-peptide; factor VIIA; gene therapy; ss. AAS11244-AAS21518 encode for novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bloactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, breast, prostate, rectal, cervical or liver tumours by comparing PRO polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to stimulate the release of tumour necrosis factor-alpha (TPF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in pericyte cells, the release of proteoglycans from of T-lymphocytes, the release of a cytokine from peripheral blood monocytes (PBMCs), or the proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify cartilage, the proliferation of inner ear utricular supporting cells or 3 Isolated, secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumours e.g. Gao Beresini M, Deforge L, Desnoyers L, Filvaroff E, Ga ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z; Claim 3; Fig 285; 813pp; English. breast, prostate, cervical 2000WO-US07377. 2000WO-US07532. 2000WO-US08439. 2000WO-US13705. 99WO-US28301. 99WO-US28634. 99WO-US28551. 2000WO-US00376. 2000WO-US03565. 2000WO-US04914. 2000WO-US05004. 99WO-US31243. 2000WO-US04341. 2000WO-US04342. 2000WO-US04414. 2000WO-US32678 **US28565** US30095 99WO-US30911 99WO-US30999 2000WO-US05004 2000WO-US05601 2000WO-US14042 US28564 2000WO-US15264 Baker KP, Beresini M, (GETH) GENENTECH INC. -SU66 2001-408281/43. -0M66 2000WO-P-PSDB; AAU12314. MO200140466-A2. 18-FEB-2000; 18-FEB-2000; 22-FEB-2000; 09-DEC-1999; 16-DEC-1999; 20-DEC-1999; 20-DEC-1999; 02-DEC-1999; 02-DEC-1999; 02-DEC-1999; 30-MAR-2000; Homo sapiens 01-DEC-2000; 06-JAN-2000; 06-JAN-2000; 24-FEB-2000; 24-FEB-2000; 01-MAR-2000; 20-MAR-2000; 21-MAR-2000; 17-MAY-2000; 30-MAY-2000; -DEC-1999; -DEC-1999; 30-DEC-1999 07-JUN-2001 Gerritsen 1 Smith V, lung,

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Human, PRO, cardiant, antiangiogenic; antiarteriosclerotic; hypotensive, vasotropic; antirtheumatic; antiarthritic; antiarfammatory; cytostatic; vulnerary; antianginal; gene therapy; cardiovascular disease; endothelial disorder; anglogenic disorder; cancer; periodontal disease;
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molecules involved in binding interactions. The polynucleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is one of seventeen nucleic acids encoding PRO polypeptides. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating cardiovascular, endothelial or antigonic disorders in a mammal. Examples of these disorders include cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arterial restenosis, Reynaud's disease, rheumatoid arthritis, angina, myocardial infarctions, thrombophlebitis and lymphangitis. The PRO polypeptides and antagonists are also used to prevent tumour angiogenesis and for treating periodontal diseases. They are also used to stimulate wound healing and tissue regeneration. The PRO nucleic acids, polypeptides and anti-PRO antibodies are useful for diagnosing a cardiovascular, endothelial or angiogenic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                               Seventeen nucleic acids encoding PRO polypeptides which are useful in diagnosis and treatment of cardiovascular, endothelial or angiogenic disorders in a mammal -
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                                                                                                                                                                                                                                                                                          KP, Ferrara N, Gerber H, Gerritsen ME;
PJ, Gurney AL, Kuo SS, Mark MR, Marsters
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 22; Length 2849;
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Pred. No. 0;
1; Mismatches
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lowski PJ, Gurney AL,
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30-NOV-1999; 99WO-US28409.
02-DEC-1999; 99WO-US28565.
16-DEC-1999; 99WO-US30095.
11-FEB-2000; 2000WO-US03565.
18-FEB-2000; 2000WO-US04341.
24-FEB-2000; 2000WO-US04342.
24-FEB-2000; 2000WO-US05841.
10-MAR-2000; 2000WO-US05841.
15-MAR-2000; 2000WO-US06884.
21-MAR-2000; 2000WO-US05883.
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llarity 99.9%;
Conservative
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Paoni NF, Pitti RM,
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Matches 1532; Conserv
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P-PSDB; AAB50952.
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                                                                                                                                                                                                      Human, PRO526, PRO719, PRO200, PRO725, PRO1031, immune related disease, inflammation, thyroiditis, demyelinating disease, skin disease,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New compositions containing a PRO526, PRO719, PRO725, PRO1031 or proteins for modulating immune response or proliferation of T-lymphocytes in mammal, especially for treating immune related disorders, e.g. graft rejection
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              TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1899
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Pred. No. 0;
1; Mismatches
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Wood WI;
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                                                                                              AAC88962 standard; cDNA; 2849
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Best Local Similarity 99.9%;
Matches 1532; Conservative
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                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                 infectious disease; ss.
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Kuo SS,
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P-PSDB; AAB49895.
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Hillan KJ,
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                                                                  CCTAAAATCGTATAAAAICTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 1443
                                                                                ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
                                                                                                                              ACCAGAACATTCTATGTACTACAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866
 regerrergrarreagriciriesaraceserrasesraarerergraegraegraeagaaaaaa 1686
                                                                                                                                                                                                                                                                                                                  Human; angiogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; angiogenic disorder; atherosclerosis; osteoporosis; hypertension; myocardial infarction; diabetic retinopathy; theumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal; ss.
                        CTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAACTCTAAAGCTCCATGTCCTGGG
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L. Hillan KJ, Kuo SS, Mark MR, Marsters SA;
Watanabe CK, Williams PM, Wood WI;
                                                                                                                                                                                                                                                                                                  Human angiogenesis-associated protein PRO200 cDNA, SEQ ID NO:50.
                                                                                                                                                      TAAACTIGIGICAIGCIGAIAGGACAGACTGGA 1536
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Pitti RM,
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P-PSDB; AAB53074.
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14-MAY-1999;
02-JUN-1999;
23-JUN-1999;
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Paoni NF, F
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PT Genetic disorders and treating cardiovascular, endothelial or angiogenic disorders and treating cardiovascular, endothelial or angiogenic disorders, such as atherosclerosis, wounds or cancer.

PT angiogenic disorders, such as atherosclerosis, wounds or cancer.

EXX claim 58, Fig 21A-B; 293pp; English.

CThe invention relates to novel human angiogenesis-associated proteins comprising a PRO proteins (AAB3504-B53097), and to nucleic acids encoding comprising a PRO mucleic acid, the recombinant production of a PRO protein. PRO antibodies specific for a PRO protein, fusion proteins comprising a PRO nucleic acid, the recombinant production of a PRO protein, and compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO compounds which inhibit the expression of a PRO protein, and compounds which inhibit the expression of a PRO protein, and compounds which inhibit the expression level of a PRO protein, or additionally encompasses methods of identifying modulators of PRO captionally encompasses methods of identifying modulators of PRO captional protein, protein, PRO additionally encompasses methods of inhibiting or stimulating endothelial or particular tissue; treating a cardiovascular, endothelial or angiogenesis of a protein, or PRO administration of a PRO protein, or an agonist or antagonist; a rectroating or stimulating endothelial captionascular, endothelial or angiogenesis via the administration of a PRO protein, or an agonist and PRO atteoporosis, myocardial infarction, hypertension, cardiopenic captiopenic disorders, such as a therrosclerosis, olders and PRO atteoporosis, myocardial infarction, hypertension, ciabetic retinopathy, rheumacoid arthritis, crown as producinon of PRO proteins, as hybridistation probes to cardiometriosis, ulcers, wounds, cancer, Alzheimer's disease, proteins, or stroke. PRO mucleic acids are additionally useful in the recombinant production of PRO proteins, to analyse genes encoding PRO proteins, to analyse g
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Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other;
Query Match
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0;

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CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483

AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA

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Human; PRO polypeptide; secreted and transmembrane protein; tumour necrosis factor-alpha; TNF-alpha; blood; proliferation; differentiation; chondrocyte; tumour; genetic disorder;
  1867 TAAACTIGIGICAIGCIGAIAGGACAGACIGGA 1899
                                                                                                                                                                                                                                                                                  cDNA encoding human PRO polypeptide #143
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98WO-US1456.
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2000WO-US04341.
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15.SEP-1999;
05.OCT-1999;
29.NOV-1999;
30.NOV-1999;
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CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGATAATA
                                                                                                                                                                                                                                                                                TTTTTGGAAGAAATCCAGAGTGGATCTGAACCTTCTAACAGGGGGGTAAGATTAT
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                                                                                                      ATGCTATAAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT
                                                                                                                                                                                                            GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CCATTITCTGGCCAGGTIGTCTCCTGGTTAAACGCTGTGGGGAACTGTGCCTGTTGTC
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                                                                              ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT
                                                                                                                                                                            GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
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New secreted and transmembrane PRO nucleic acids, useful for gene therapy, in chromosome and gene mapping, as chromosome markers, in tissue typing, and in chromosome identification -
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ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
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Smith V, Ste
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for modulating biological activities of cells expressing PRO polypeptides, and for identifying agonists or antagonists.

The PRO polypeptides are useful for for stimulating the release of tumour necrosis factor (TMF)-labha from human blood, for stimulating the proliferation or differentiation of chondrocytes, and detecting the presence of tumours. The polymolecitide sequences encoding PRO polypeptides are useful as hybridisation probes, in chromosome and gene mapping, in the generation of antisense RNA and DNA, in the preparation of PRO polypeptides, for generating transgenic animals or knockout animals, for the genetic analysis of individuals with genetic disorders, and in gene therapy. ACA03803-ACA03877 represent cDNAs encoding the human PRO polypeptides of the invention.

Note: The sequence data for this patent was obtained in electronic format directly from the USPTO web site at ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACGGTA 1086 723 426 486 183 546 243 909 363 423 543 999 AATATITITCCTTCTGAACCAGGGTTCTGCATCACTACAACATTGTCATGCCACAATTCA 786 483 847 ArgeraraAcrecerrraGracerregaaGacerrarregarecragaGagagar 906 603 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 966 TITITGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 663 CCATTITCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC 783 63 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGAGAAAATGTATGGATACAAC CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 367 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC TTACGTTTGATGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATT TTGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGGTTCTGGTA CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA cadadecreteredecreteredecreteredecriredecatedecreterata GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC TTACGTTTGATGAAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATT **ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAG** 4 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA Gaps DB 25; Length 2849; ö 0; Indels Sequence 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other; Score 1532.6; 99.9%; Pred. No. 0; ive 1; Mismatches 99.88; Query Match Best Local Similarity 99.9 Matches 1532, Conservative 1027 64 124 487 547 244 603 304 667 364 727 424 787 484 544 907 604 967 664 724 184 \$ ò 셤 ò g à 셤 à g ò 셤 ठे a ò 셤 ઠ 셤 à 셤 ð g ठे 셤 δ 셤 8

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(GETH) GENENTECH INC.

Gao W; Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, G: Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-331925/31. P-PSDB; ABU66988.

New secreted and transmembrane nucleic acids and polypeptides, designated as PRO, useful for treating inflammation, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, AIDS, or cancer

Claim 2; Fig 285; 659pp; English.

The invention relates to an isolated nucleic acid comprising, or which is at least 80% identical to, or the full-length coding sequence of, any of the 275 nucleotide sequences, encoding the corresponding PRO polypeptide (one of 275 secreted or transmembrane proteins). The nucleic acid further comprises the full-length coding sequence of the DNA deposited curther comprises the full-length coding sequence of the DNA deposited given in the specification. Also included are vectors and host calls for producing PRO proteins, PRO fusion proteins, anti-PRO actionates and mature sequences, methods of detecting PRO proteins, methods for stimulating the release of TNF-alpha (tummur necrosis factor alpha) from human blood, and the proliferation of differentiation of fundrocyte cells, the release or proliferation of, or gene expression in pericyte cells, the release or proteoglycans from cartilage, proliferation of fundrocyte cells, the release of cytokine from peripheral blood monounclear cells, the release of a cytokine from peripheral blood monounclear cells, the release of proliferation of endothelial cells, a method for modulating the uptake of glucose or free fatty acid (FFA) by skeletal muscle cells, cor the differentiation of adipocyte cells, a method for inhibiting the bluding of A-pepting to factor VIIA, or the differentiation of adipocyte cells, a method for detecting the proliferation of adipocyte cells, a method for detecting cor from any of the nucleocities sequences cited above The nucleic acids and colypeptides are useful for treating inflammatory diseases, organ farm and any perhanement of failure, atherosclerosis, cardiac injury, infertility, birth defects, or premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or

c complications. The nucleic acids are useful as hybridisation in chromosome and gene mapping, and in generating antisense RNA the polypeptides are useful as pharmaceuticals, diagnostics, ors or bioreactors. Both are useful in tissue typing. sent sequence encodes a PRO protein of the invention. e 2849 BP; 851 A; 528 C; 619 G; 850 T; 1 other; h 99.8%; Score 1532.6; DB 25; Length 2849; Similarity 99.9%; Pred. No. 0;	532	9	64 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATC 123	24 CAAGAAATACGGTCTTGGTATGGAGATTAGTAGGGGTAGAGGAAAATGTATGGATACAAC 183 	84	44 TIGIAGAAGITGAGGAACCCAGIGAIGGAACTAIATIAGGGGGCTGGTGTGGTTA 303	04 CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363 	64 AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 423 	24 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 483	B4 AIGCIATAACIGCCITIAGIACCITGGAAGACCITAITCGAIATCITGAACCAGAGAGAF 543 	44	04 TITITGGAAGAAARTCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 663 	664 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACGGATA 723 		184 TCCACAATTGCAATGAATGTCAATGTCCCAAGCAAAGTTACTAAAAATACCACGAGG 843	44 TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG 903	7 T 0
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10-MAY-2001; 2001WS-0866034.
25-MAY-2001; 2001WS-0866034.
25-MAY-2001; 2001WS-0866034.
25-MAY-2001; 2001WS-0866036.
19-JUN-2001; 2001WS-0866036.
19-JUN-2001; 2001WS-086636.
19-JUN-2001; 2001WS-086636.
19-JUN-2001; 2001WS-0886379.
18-JUN-2001; 2001WS-0987879.
18-JUN-2001; 2001WS-0987879.
16-JUN-2001; 2001WS-0987879.
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19-DEC-2001; 2001US-0028072 (GETH) GENENTECH INC.

Gao W; Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-148238/14. P-PSDB; ABU59793.

Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer

Claim 2; Fig 285; 659pp; English

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in complete are useful in detecting PRO polypeptides in a sample, in complete a biological activity of a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO colypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus complete. PRO1312 stimulates hypertrophy of neonatal heart and is thus complete. PRO1312 stimulates hypertrophy of neonatal heart and is thus stimulate adrenal cortical capillary endothelial growth, and PRO136, PRO136, pRO136, pRO136, pRO136, pRO136, pRO136, pRO136, pRO136, proders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating conditions or disorders melgingly properties are calculated protiferation of endothelial growth in the protiferation of mammals which would be beneficial in inhibiting tumour growth. PRO826, pro136, and PRO136 stimulated proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO1068 or PRO1132 enhance survival/proliferation of cells in and in naurons cells (PRO1312 is also enhances survival/proliferation of disorders of injuries, e.g. returnlist pigmentoeum, AMD. PRO819, pro826, and therefore are useful for treating the proliferation of mammalian kidney meanigial cells, and therefore are useful for treating sports injuries, and arthritis. This sequence encodes a novel human PRO protein.

s ys	T; 1 other;
Query Best] Match	y Match 99.8%; Score 1532.6; DB 25; Length 2849; Local Similarity 99.9%; Pred. No. 0; hes 1532; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
ď	4 GTABATTCCAGCTACCAGCAACAAGGAACAGAACGGAACG
q	367 GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA 426
ð í	4 GAAITATTACTGTGTGTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC
g ò	AC 18:
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<i>&</i> :	84 TTACGTTTGAAGATTTGGGCTTGAAGACCCAGAAGATGACATATGCAAGTATGATT 24
đ	T 60
රු සි	244 ITGTAGAAGTTGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGGTTCTGGTA 303
ò	304 CIGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363
තු	
\$ 6	364 AATATTTTCCTTCTGAACCAGGGTTCTGCATCCACTACAACATTGTCATGCCACAATTCA 423
3 2	A CACAMICATION CACAMICA CACAMI
경 음	87 CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA 84
ò	484 AIGCIATAACIGCCITIAGIACCIIGGAAGACCIIAIICGAIAICIIGAACCAGAGAGAI 543
qq	847 AIGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT 906
ζ	544 GGCAGTHGGACHTAGAAGATCHATATAGGCCAACTTCTTGGCAACTTTTG 603
đ	907 GGCAGTIGGACTIAGAAGAICIAIAIAAGGCCAACTIGGCAACTICTIGGCAAGGCTITIG 966
රු සි	604 TITITGGAAGAAAATCCAGAGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATAT 663
ò	TGCACACCTCGTAACTTCTCAGTGTCCCATAAGGGGAAGGAA
qa	1027 ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 1086
λō	724 CCATTITCTGGCCAGGITGTCTCCTGGTTAAACGCTGTGGGAACTGTGCCTGTTGTC 783
qa	1087 CCATTITCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAAACTGTGCCTGTTGTC 1146
ò	84 TCCACAATTGCAATGAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACACGAGG 8
qq	cacaattecaateaatetcaateteteeceaaecaaettactaaaaata
ò	844 TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG 903
q	cricadiidadaccaaadaccddigicaddagaaiidcacaaaicacicad
ķ	04 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGCAGAGGAGGAGCACGAGGAGGATAGCCGC 96
අු	1267 CCCTGGAGCACCATGAGGAGTGTGACTGTGTGTGCAGAGGGAGCACAGGAGGATAGCCGC 1326
ò	64 ATCACCACCAGGAGCTCTTGCCCAGAGCTGTGCAGTGGCTGATGTTTTATAGAGAA 102:
qq	1327 Arcaccadcadcretracccadadcreracadardcadredcrartcharradada 1386

Š	1024	CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1083
qa	1387	CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1446
ò	1084	GATTTACAGTGCATTCTGAAAGAGGACATCAAACAGAATTAGGAGTTGTGCAACAGCT 1143
qa	1447	GATTTACAGTGCATTCTGAAAGAGGAGACATCAACAACAGAATTAGGAGTTGTGCAACAGCT 1506
ò	1144	CTTTTGAGAGGAGGCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAAAAATTAA 1203
qq	1507	CITTTGAGAGGCCTAAAGGACAGGAGAAAAGGTCTTCAATCGTGGAAAGAAA
ά	1204	ATGTTGTATTAAATAGATCACCAGCTAGTTTCAGAGTTACCATGTACGTATTCCACTAGC 1263
qa	1567	ALGITICINITALATABATCACCAGCTAGTITCAGAGTTACCATGTATCCACTATCATAGC 1626
ζ	1264	TGGGTTCTGTATTTCAGTTCTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAA 1323
qa	1627	TGGGTTCTGTATTTCAGTTCTTTTCGATACGGCTTAGGGTAATGTCAGTACAGGAAAAAAAA
ò	1324	CIGTGCAAGTGAGCACCTGATTCCGTTGCCTTAACTCTAAAGCTCCATGTCCTGGG 1383
qq	1687	CHGIGHTHING CONTROLL
δλ	1384	CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTT
qq	1747	CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTT
ò	1444	ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
qq	1807	ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866
δλ	1504	TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
QQ	1867	TARACTIGICALGATAGGACAGACTGGA 1899

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APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
APPLICANT: Kuo, Sophia S.
TITLE OF INVENTION: NOVEL POLYPEPTIDES HAVING HOMOLOGY TO VASCULAR
TITLE OF INVENTION: EMDOTHELIAL CELL GROWTH FACTOR AND BONE MORPHOGENETIC
TITLE OF INVENTION: PROTEIN 1 AND NUCLEIC ACIDS ENCODING SAME, THEIR USES,
TITLE OF INVENTION: AND PROCESSES FOR THEIR PRODUCTION
FILE REPERENCE: P1122
CURRENT APPLICATION NUMBER: US/09/040,220D
CURRENT APPLICATION DATE: 1998-03-17
NUMBER OF SEQ ID NOS: 8
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US-08-062-632-4
US-08-781-891-207
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US-08-738-349-1
US-08-749-522-6
US-09-041A-1
US-09-099-041A-1
US-09-207-359B-1
US-09-207-359B-1
US-09-340-620A-1
US-09-340-620A-1
US-08-418-1
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; Patent No. 6391311
; GENERAL INFORMATION:
LOCATION: 2689
OTHER INFORMATION: N is A,
    ORGANISM: Human
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JOHNSON LINCOLLAND.

APPLICANT: Kuo, Sophia S.

TITLE OF INVENTION: POLYPEPTIDES HOWOLOGOUS TO VEGF AND BMP:
FILE REFREENCE: P1122B.

CURRENT APPLICATION NUMBER: US/09/265,686

CURRENT FILING DATE: 1999-03-10

PRIOR FILING DATE: 1999-03-17

PRIOR FILING DATE: 1998-11-02

PRIOR FILING DATE: 1998-11-02

NUMBER: OF SEQ ID NOS: 8

SEQ ID NO I.
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US-09-265-686-1
Sequence 1, Application US/09265686
Parent No. 6455283
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: Unknown
LOCATION: 2689
OTHER INFORMATION: Any nucleotide
                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
FEATURE:
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US-09-265-686-1
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CAGAAGCTGTGAGTCCTTCAGTGCTACCCCCTTCAGCTTTGCCACTGGACCTGCTTAATA
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| Patent No. 6495668 |
| GENERAL INFORMATION: |
| APPLICANT: Gilbert, Teresa |
| APPLICANT: Hart, Charles E. |
| APPLICANT: Hart, Charles E. |
| APPLICANT: Hart, Charles E. |
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| APPLICANT: Hart, Charles E. |
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Best Local Similarity 99.8
Matches 1522; Conservative
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; LOCATION: (154)...(1191)
US-09-564-595D-32
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ORGANISM: Homo sapiens
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                              ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAGAT
                                                                                                     GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
                                                                                                                                                       GCCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
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GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Piddington, Christopher

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APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertagon, Debra G.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REFERENCE: 98-60C1
CURRENT PILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR PILING DATE: 2000-03-31
NUMBER OF SEC ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEC ID NO 1
LEARTH: 1760
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98.4%; Score 1511; D
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches
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                                                                                                                                                           Length 1764;
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NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                           97.5%;
                                                                                                                                                           Query Match
Best Local Similarity 99.5'
Matches 1522; Conservative
                                                                                                 NAME/KEY: CDS
| LOCATION: (154)...(1191)
US-09-457-066-1
                           SEQ ID NO 1
LENGTH: 1760
TYPE: DNA
ORGANISM: Homo sapiens
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Batent No. 6432673

GENERAL INFORMATION:
APPLICANT: Baco, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
TITLE DO INVANTION: GROWTH FACTOR HOMOLOG ZVE)
TITLE PEFERENCE: 98-60
CURRENT FILING DATE: 1999-12-07
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                                                                GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
                                                                                GTABARTTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
                                                                                                                                                                                          CAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAAATGTATGGATACAAC
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                                Gaps
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 Length 1095;
                               Indels
Score 955.6; DB 4;
Pred. No. 9.8e-259;
1; Mismatches 0;
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 Query Match 62.2%;
Best Local Similarity 99.9%;
Matches 955; Conservative
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US-09-706-968-50
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    AGAACGTATGCGTTATCTCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCT
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GENERAL INFOGRATION:
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Shedington, Christopher S.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: Glibertson, Debra G.
APPLICANT: GROWTH FACTOR HOMOLOG ZVE
FILE REREBERCE: 99-12-07
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SEQ ID NO 50
LENGTHARE: FastSEQ for Windows Version 3.0
LENGTH: 1095
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ORGANISM: Artificial Sequence
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US-09-457-066-50
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46.9%; Score 721; DB 4; Length 35
Best Local Similarity 83.6%; Pred. No. 1.4e-192;
Matches 817; Conservative 0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 34, Application US/09564595D
Patent No. 649568
GENERAL INPORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Teresa
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
SPRIOR FILING DATE: 1999-11-10
FRIOR FILING DATE: 1999-11-10
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; LOCATION: (1049)...(2086)
US-09-564-595D-34
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ORGANISM: Mus musculus
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                                 APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles B.
APPLICANT: Hart, Charles B.
APPLICANT: Piddington, Christopher S.
APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TILLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGFS
FILLE REFERENCE: 98-601
CURRENT FILING DATE: 2000-11-06
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FactsEQ for Windows Version 3.0
SSOFTWARE: FactsEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA
ORGANISM: Artificial Sequence
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                  GENERAL INFORMATION
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                                                                                                         Score 721; DB 4; I
Pred. No. 1.4e-192;
0; Mismatches 160;
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Best Local Similarity 83.6%;
Matches 817; Conservative
; FEATURE:
; NAMBKEX: CDS
; LOCATION: (1049)...(2086)
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Patent No. 6432673;
GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hart, Charles E.
APPLICANT: Shoemaker, Faul O.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Shoemaker, Kimberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
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APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: BERERENCE: 98-60
CURRENT APPLICATION UNDMER: US/09/457,066
CURRENT APPLICATION UNDMER: US/09/457,066
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CURRENT APPLICATION UNDMER: US/09/457,066
CURRENT APPLICATION UNDMER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
MUMBER OF SEQ ID NOS: 50
SOFTWARE: PastSEQ for Windows Version 3.0
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OTHER INFORMATION: n = A,T,C or G
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Matches 547;
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US-09-457-066-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            184 TIACGITIGAIGAAAGAITIGGGCITGAAGACCCCAGAAGAIGACAIAIGCAAGIAIGAIT 243
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TIGIAGAAGITGAGGAACCCAGTGATGGAACTATATTAGGGCGCTGGTGGTTCTGGTA 303
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    544 GCCAGIIGGACTIAGAAGAICIATAIAGGCCAACIIGGCAACIICIIGGCAAGGCIITIIG 603
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Pred. No. 1.4e-192;
0; Mismatches 160; Indels
                                                                                                                                                                                                                                                                                              Sequence 42, Application US/09457066

Patent No. 6432673

GENERAL INFORMATION:

APPLICANT: Hart, Charles B.

APPLICANT: Biddington, Christopher S.

APPLICANT: Biddington, Christopher S.

APPLICANT: Bhogmard, Paul O.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Shoemaker, Kimberly E.

APPLICANT: Glibertson, Debra G.

APPLICANT: Glibertson, Debra G.

APPLICANT: West, James W.

TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3

FILLE REPRENCE: 98-60.

CURRENT APPLICATION NUMBER: US/09/457,066

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50

SEQ ID NO 42

SEQ ID NO 553
                                                                                                  2091 AGCCTTCGTAGCAGCAC 2107
                      964 ATCACCACCAGCAGCTC 980
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Best Local Similarity 83.6%;
Matches 817; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; NAME/KEY: CDS
; LOCATION: (1049)...(2086)
US-09-457-066-42
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ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: 2
OTHER INFORMATION: 2
NAME/KEY: misc feature
LOCATION: (1)...(1035)
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Best Local Similarity 57.5%; Pred. No. 1.5e-182;
Matches 547; Conservative 239; Mismatches 166;
CURRENT APPLICATION NUMBER: US/09/706,968
CURRENT FILING DATE: 2000-11-06
PRIOR APPLICATION NUMBER: US/09/541,752
PRIOR FILING DATE: 2000-03-31
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 6
LENGTH: 1035
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                                                                                                             567 NATHWSNGGNGTNWSNTAYAAYWSNCCNWSNGTNACNGAYCCNACNYTNATHGCNGAYGC 626
                    801 NAARMGNTAYWSNTGYACNCCNMGNAAYTAYWSNGTNAAYATHMGNGARGARYTNAARYT
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US-09-540-224-3

is Sequence 3, Application US/09540224

is Sequence 3, Application US/09540224

is General No. 6468543

is General No. 6468543

is General No. 6468543

is General No. 6468543

is General No. 6468543

is General No. 6468543

is TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

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is TITLE OF INVENTION: LIGAMENT AND CARTILAGE USING ZVEGF4

is CURRENT FILING DATE: 2000-03-31

is EARLIER FILING DATE: 2000-03-31

is CURRENT FILING DATE: 2000-02-04

in NUMBER OF SEQ ID NOS: 9

is SOFTWARE: FastSEQ for Windows Version 3.0

is LENGTH: 1472

it TYPE: DNA

CORMANISM: Mus musculus

CORMANISM: Mus musculus
                                                                              NAME/KEY: CDS
LOCATION: (93)...(1205)
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                                         TCATACTTATCCAAGAAATACGGTCTTGGTATGGAGATTAGTAGCAGTAGAGGAAATGT 172
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Patent No. 649568

GENERAL INFORMATION:
APPLICANT: Glabert, Teresa
APPLICANT: Bleppard, Paul O.
APPLICANT: Bleppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/564,595D
CURRENT APPLICATION NUMBER: US 09/304,216
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FLING DATE: 1999-05-03
PRIOR FLING DATE: 1999-01-10
PRIOR APPLICATION NUMBER: US 60/164,463
PRIOR FLING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
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LOCATION: (1)...(1110)
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7.6%; Score 117.4; DB 4; Length 1472;
Best Local Similarity 50.8%; Pred. No. 3.4e-23;
Matches 493; Conservative 1; Mismatches 402; Indels 75;
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GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Hart, Charles E.
APPLICANT: Sheppard, Paul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
                                                                                                                           FILE KEFARANCE: 37-12
CURRENT PELICATION NUMBER: US/09/564,595D
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-05-03
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 1999-11-10
PRIOR FILING DATE: 2000-02-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FASTSEQ for Windows Version 4.0
SSOFTWARE: FASTSEQ for Windows Version 4.0
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ORGANISM: Mus musculus
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LOCATION: (93)
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                                         837 CACGAGGICCITCAGITGAGACC-----AAASACCGGIGICAGGGGATIGCACAAA 887
                                                       948 ACAGGAGGATA 958
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Search completed: November 26, 2003, 05:52:18 Job time : 81.0293 secs

Run

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TYPE: DNA
ORGANISM: Homo sapiens
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Best Local Similarity
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-10-131-600-4
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US-09-978-295A-487
US-09-99-825A-487
US-09-99-832A-487
US-09-99-832A-487
US-09-99-832A-487
US-09-978-08A-487
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US-09-998-919-487
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Maximum Match 100%
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APPLICANT: BERKSSON, U1f

APPLICANT: BERKSSON, U1f

APPLICANT: AASE, Kaxin

APPLICANT: DEE, Xuri

APPLICANT: DEE, Xuri

APPLICANT: DINTELA, Marko

APPLICANT: DISTANO, Annica

APPLICANT: DISTANO, Annica

APPLICANT: DISTANO, Annica

APPLICANT: DISTANO, Annica

APPLICANT: DISTANO, Annica

APPLICANT: BETSENCITZ, Christer

ITILE OF INVENTION: THEREFOR, AND USES THEREOF

ITILE OF INVENTION: THEREFOR, AND USES THEREOF

ITILE OF INVENTION: THEREFOR, AND USES THEREOF

TILE REPRESENCE: 09-410349-Eriksson et al-1064-44740

CURRENT APPLICATION NUMBER: 00/10, 349

PRIOR FILING DATE: 1999-09-09

PRIOR FILING DATE: 1998-12-03

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1998-12-18

PRIOR FILING DATE: 1999-05-21

PRIOR PELICATION NUMBER: 60/113,002

PRIOR FILING DATE: 1999-07-15

NUMBER OF SEQ ID NOS: 39

SOFTWARKE: PATCHLIN VEY: 2.0

SEQ ID NO 4

LENGTH: LS36
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Patent No. US20020164687A1
GENERAL INFORMATION:
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Length 1536;

DB 10;

Score 1535.6; Pred. No. 0;

100.0%;

Qy 1081 CAGGATTTACAGTGCATTCTGAAAGAGACATCAAACAGAATTAGGAGTTGTGCAACA 1140 Db 1081 CAGGATTTACAGTGCATTCTGAAAGAGACATCAAACAGAATTAGGAGTTGTGCAACA 1140 Db 1081 CAGGATTTACAGTGCATTCTGAAACAGAAATAGATTCAGAATTAGGAGTTGTGAACAGAAAT 1200 Qy 1141 GCTCTTTTGAGAGGAGCCTAAAGAGAAAAGGTCTTCAATCGTGGAAAAAAT 1200 Db 1201 TAAATGTTGATTAAATAGATCACCAGTTACAGAATTACAATGATCCACTACTACAGAAAA 1200 Db 1201 TAAATGTTGTATTAAATAGATCCTTTCCATTACAGAATTACAATACATCACTACAGAAAA 1200 Qy 1261 AGCTGGGTTCTGTATTCAGTTCTTTCCATTACGAGTTACACATACACAACACACAC	RESULT 2 UG-111-600-4 Sequence 4, Application US/10131600 Sequence 4, Application US/10131600 Sequence 4, Application No. USZ0030082670A1 GENERAL INPORMATION: APPLICANT: ERIKSSON, UIF APPLICANT: LEE, Kuri APPLICANT: LEE, Kuri APPLICANT: PONTEN, Annica APPLICANT: PONTEN, Annica APPLICANT: OSTETNA, Annica APPLICANT: OSTETNA, Annica APPLICANT: OSTETNA, Annica APPLICANT: OSTETNA, Annica APPLICANT: OSTETNA, Annica APPLICANT: OSTETNA, AND USES THEREOF FILE OF INVENTION: PLATELET-DERIVED GROWTH PACTOR C, FILE OF INVENTION: PLATELET-DERIVED GROWTH PACTOR C, FILE OF INVENTION: PLATELET-DERIVED GROWTH PACTOR C, FILE OF INVENTION: PLATELET-DERIVED GROWTH PACTOR C, FILE OF INVENTION: PLATELET-DERIVED GROWTH PACTOR C, FILE OF INVENTION: PLATELET-DERIVED GROWTH PACTOR C, FILE NEERRINGE: 09-410349 OF PRIOR FILING DATE: 1998-10-30 OF PRIOR FILING DATE: 1998-10-10 OF PRIOR FILING DATE: 1998-10-10 OF PRIOR FILING DATE: 1998-10-10 OF PRIOR FILING DATE: 1998-10-10 OF PRIOR FILING DATE: 1998-10-10 OF PRIOR FILING DATE: 1998-10-10 OF PRIOR FILING DATE: 1998-10-11 OF PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR PRIOR DATE: 1998-10-11 OF PRIOR
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                                   CAGGATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACA
DB 14; Length 2825
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Publication No. US20030113870A1
GENERAL INFORMATION:
APPLICANT: Ferrar Napoleone
APPLICANT: FOLO. Sophia S.
TITLE OF INVENTION: POLYERTIDES HOMOLOGOUS TO TITLE OF INVENTION: POLYERTIDES HOMOLOGOUS TO TITLE OF INVENTION UNMER: US/10/178,442;
CURRENT APPLICATION NUMBER: US/20/265,686;
PRIOR APPLICATION NUMBER: US 09/265,686;
PRIOR FILING DATE: 1999-03-10
PRIOR FILING DATE: 1998-01-02;
PRIOR FILING DATE: 1998-03-17;
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PATENTING VERSION 3.1
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99.8%; Score 1532.6;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches
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LOCATION: (2689)..(2689)
OTHER INFORMATION: Any nucleotide
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         Query Match 100.0%; Score 1535.6; Best Local Similarity 100.0%; Pred. No. 0; Matches 1536; Conservative 0; Mismatches
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64 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 123 401 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 460 402 GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC 460 124 CAAGAAATACGGTCTTGGTATGGAATTAGTAGCAGTAAGAAGTATTGGATACTACT 125 CAAGAAATACGGTCTTGGTATGGAATTAGTAGCAGTAAGAAGAATACTAATC 520 126 CAAGAAATACGGTCTTGGTATGGAATTAGTAGCAGTAAGAAATGTATGAATACAAT 127 CAGAAATTGGACTTTGGGCTTGAAGACTAATAGAGCAATATGAAGTATGATT 580 241 TTGTAGAAGTTGAGGAACCCAGTGAAGACCCAGAAGAGTATTGAATTAGTAGAATTAGTAGAAGTTGAAGTATTAGATTAGAAGTTAGAAGTTGAAGTATTAGAAGA	

NUMBER: 60/066364 1997-11-21 1998-101-0 1998-03-10 1998-03-11 NUMBER: 60/077641 1998-03-11 1998-03-11 1998-03-11 NUMBER: 60/077649 1998-03-11 NUMBER: 60/077649 1998-03-12 NUMBER: 60/077649 1998-03-12 NUMBER: 60/07791 1998-03-12 NUMBER: 60/07791	73.50.70.70.70.70.70.70.70.70.70.70.70.70.70	
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION WUMBER: 60/08138
PRIOR APPLICATION WUMBER: 60/08138
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Gerber, Hanspeler
Gerritsen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
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APPLICANT: Baker Kevin P.
APPLICANT: Botetein, David
APPLICANT: Botonyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
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APPLICATION NUMBER: 60/084441
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APPLICATION NUMBER: 60/080328
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            Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
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Gao, Wel-Qiang
Gerber, Hanspeter
Gerriteen, Mary B.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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APPLICATION NUMBER: 60/079728
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Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Ashkenazi, Avi
Baker Kevin P.
Botstein, David
Desnoyers, Luc
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APPLICATION NUMBER: 60/078936
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APPLICATION NUMBER: 60/080105
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APPLICATION NUMBER: 60/080328
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APPLICATION NUMBER: 60/081229
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APPLICATION NUMBER: 60/081819
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                                                                                                                                                                                             1807 ACCAGAACATICTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1866
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APPLICANT: William I.
APPLICANT: Wood, William I.
IITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
IITLE OF INVENTION: Acids Encoding the Same
                                                                                                                                               ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT
                                                                                                                                                                                                                                             TAAACTIGIGICAIGCIGAIAGGACAGACIGGA 1536
                                                                                                                                                                                                                                                                              THILE OF INVENTION: ACCOUNTING THE SAME CURRENT APPLICATION NUMBER: US/09/999, 832A CURRENT APPLICATION NUMBER: US/09/999, 832A CURRENT APPLICATION NUMBER: 09/918565 PRIOR APPLICATION NUMBER: 09/918565 PRIOR PELING DATE: 2001-07-30 PRIOR PELING DATE: 1997-10-17 PRIOR APPLICATION NUMBER: 60/064249 PRIOR FILING DATE: 1997-11-03 PRIOR APPLICATION NUMBER: 60/065311 PRIOR APPLICATION NUMBER: 60/06534 PRIOR FILING DATE: 1997-11-21 PRIOR APPLICATION NUMBER: 60/077450 PRIOR FILING DATE: 1998-03-10 PRIOR PILING DATE: 1998-03-11 PRIOR PILING DATE: 1998-03-11 PRIOR PILING DATE: 1998-03-11 PRIOR PILING DATE: 1998-03-11 PRIOR PILING DATE: 1998-03-11 PRIOR PILING DATE: 1998-03-11 PRIOR APPLICATION NUMBER: 60/077641 PRIOR APPLICATION NUMBER: 60/077641 PRIOR APPLICATION NUMBER: 60/077641 PRIOR APPLICATION NUMBER: 60/077641 PRIOR APPLICATION NUMBER: 60/077641 PRIOR APPLICATION NUMBER: 60/077641 PRIOR PILING DATE: 1998-03-11
                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 487, Application US/09999832A Publication No. US20020192706A1 GENERAL INFORMATION:
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
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APPLICATION NUMBER: 60/078004
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Paoni, Nicholas F.
Roy, Margaret Ann
Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Filvaroff, Ellen
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Gerritsen, Mary E
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Kuo, Sophia S.
Napier, Mary A.
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Desnoyers, Luc
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APPLICANT: Baker Kevin P
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1387 CGTATGCGTTATCTCCATCCTTAATCTCGGTTGTTTGAAGGACCTTTCATCTTCAGG 1446
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                                                                                                   1384 CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAA
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CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Godowski, Paul J.
Grimaldi, J. Christopher
Hillan, Kenneth J
Kljavin, Ivar J.
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US-09-978-189-487
US-09-978-189-487
Sequence 487, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
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Botstein, David
Desnoyers, Luc
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Tumas, Daniel
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PRIOR APPLICATION NUMBER: 60/065311
PRIOR PLING DATE: 1998-03-10
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APPLICATION NUMBER: 60/081195
FILING DATE: 1998-04-08
APPLICATION NUMBER: 60/081203
FILING DATE: 1998-04-09 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080333 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/080334 FILING DATE: 1998-04-01 APPLICATION NUMBER: 60/081070 FILING DATE: 1998-04-08 APPLICATION NUMBER: 60/081049 APPLICATION NUMBER: 60/081071 FILING DATE: 1998-04-08

3ER: 60/081223 38-04-09 3ER: 60/08195 38-04-15 3ER: 60/08181 38-04-15 38-04-15 38-04-15 38-04-15 38-04-15 38-04-15 38-04-15 38-04-15 38-04-15 38-04-15	NUMBER: 60 1998-04-2 1998-04-2 1998-04-2 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60 1998-04-2 NUMBER: 60	1998-04-29 1998-04-29 1998-04-29 1998-04-29 1998-04-29 1998-04-29 1998-04-29 1998-04-30 1998-04-30 1998-04-30 1998-04-30 1998-04-30 1998-05-05 1998-05-06 1998-05-06 1998-05-06 1998-05-06 1998-05-07
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PRIOR APPLICATION NUMBER: 60/085323
PRIOR APPLICATION NUMBER: 60/085582
PRIOR FILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/08569
PRIOR FILING DATE: 1998-05-15
PRIOR PILING DATE: 1998-05-15
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PRIOR APPLICATION NUMBER: 60/08550
PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/085573
PRIOR FILING DATE: 1998-05-15
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PRIOR FILING DATE: 1998-05-15
PRIOR FILING DATE: 1998-05-15
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Best Local Similarity 99.9
Matches 1532; Conservative 4 367 64 427 124 487 547 244 607 304 364 727 424 787 484 847 544 604 196 664 184 667 724 q 승 유 8 6 6 6 8 8 8 8 8 8 8 8 8 ò 8 6 6 6 A 4 ð

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APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J
APPLICANT: Hillan, Kenneth J
APPLICANT: Kuo, Sophia S.
APPLICANT: Ruo, Sophia S.
APPLICANT: Pan, James;
APPLICANT: Pan, James;
APPLICANT: Roy, Margaret Ann
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Wolliams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Wolliams, P. Mickey
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION: Acids Encoding the Same
TITLE OF INVENTION NUMBER: US/09/978,608A
CURRENT APPLICATION NUMBER: US/09/978,608A
CURRENT APPLICATION NOWBER: US/09/978,608A
CURRENT APPLICATION NOWBER: US/09/978,608A
FILE REPREMENTED NOS: 624
PRIOR APPLICATION NOWBER: US/09/978,008A
FILE REPREMENTED NOS: 624
PRIOR APPLICATION NOWBER: US/09/978,008A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: unknown base US-09-978-608A-487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: unsure
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                                                                       1087 CCATTITCTGGCCAGGTIGTCTCCTGGTTAAACGCTGTGGTGGCAACTGTGCCTGTTGTC 1146
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                                                  TCCACAATTGCAATGTCAATGTGTCCCAAGCAAAGTTACTAAAAAATACCACGAGG
                                                                                                                                TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGACGTGG
                                                                                                                                                                                                            Sequence 487, Application US/09978608A; Bublication No. US20030045462A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Borstein, David
APPLICANT: Berstein, David
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Ferrara, Napoleon
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gacher, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Audrey
APPLICANT: Goddwski, Paul J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
US-09-978-608A-487
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APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Ford, Sherman
APPLICANT: Garitsen, Mary E.
APPLICANT: Garritsen, Mary E.
APPLICANT: Garritsen, Mary E.
APPLICANT: Gardard, Audrey
APPLICANT: Gardard, Audrey
APPLICANT: Garmeld, J. Christopher
APPLICANT: Garmeld, J. Christopher
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Roy, Sophia S.
APPLICANT: Napier, Mary S.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Shelton, David L.
APPLICANT: Shelton, David L.
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, P. Mickey
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Daniel
APPLICANT: Williams, Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630PLCIS
FILE REFERENCE: P260PLCIS
MUMBER OF SEQ ID NOS: 624
NUMBER OF SEQ ID NOS: 624
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION: unknown base US-09-978-585A-487
Baker Kevin P.
Botstein, David
Desnoyers, Luc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Prior Application removed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: unsure
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                                                       ACAGCTGCACACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA
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Sequence 487, Application US/09978585A Publication No. US20030049633A1 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi

RESULT 10 US-09-978-585A-487

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APPLICANI: Wood, Williams, P. Mickey
APPLICANI: Wood, Williams, P. Mickey
ITILE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REPRENCE: P2630PLG4
CURRENT APPLICATION NUMBER: US/09/978,191A
CURRENT FILING DATE: 2001-10-15
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FUBLICATION No. US20030050239A1
GENERAL INFORMATION:
APPLICANT: Bakenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Etnza, Napoleon
APPLICANT: Filvaroff, Ellen
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Goddwski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
Pan, James;
Pani, James;
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Shelton, David L.
Stewart, Timothy A.
Tumas, Daniel
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Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
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Filvaroff, Ellen
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367 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA 426 4 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA Gaps Query Match 99.8%; Score 1532.6; DB 11; Length 2849; Best Local Similarity 99.9%; Pred. No. 0; Matches 1532; Conservative 1; Mismatches 0; Indels 0; PRIOR APPLICATION NUMBER: 60/083495
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Goddard, Audrey
Goddowski, Paul J.
Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J
Kljavin, Ivar J.
Kuo, Sophia S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 487, Application US/09978564A Publication No. US20030050241A1 GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ferrara, Napoleon
Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
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Roy, Margaret Ann
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Gerber, Hanspeter
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Botstein, David
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APPLICATION NUMBER: 60/081203 FILING DATE: 1998-04-09 APPLICATION NUMBER: 60/081229

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dinaldi, O'Chris.

Handli, O'Chris.

Handli, O'Chris.

Roy, Mastan L.

Hand, Millam, Para J.

Tr. Thurst, David L.

Tr. Tr. Thurst, David L.

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Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
Botstein, David
Desnoyers, Luc
Eaton, Dan
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Grimaldi, J. Christopher
Gurney, Austin L.
Hillan, Kenneth J.
Kljavin, Ivar J.
Kuo, Sophia S.
Napier, Mary A.
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Filvaroff, Ellen
Fong, Sherman
Gao, Wei-Qiang
Gerber, Hanspeter
Gerritsen, Mary E.
Goddard, Audrey
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Shelton, David L.
Stewart, Timothy A.
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Paoni, Nicholas F.
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APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
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| cgnn2_6/ptodata/2/pna/US100A_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US101B_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US104B_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US104B_COMB.seq: |
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| cgnn2_6/ptodata/2/pna/US104B_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US6001_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US6011_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US6011_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US6012_COMB.seq: |
| cgnn2_6/ptodata/2/pna/US6013_COMB.seq: |
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/cgn2_6/ptodata/2/pna/US6047_
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli
ΩI	1 PCT-US99-22668-4 2 PCT-US99-22668-4 21 US-09-410-349A-4 35 US-09-852-209-4
DB	1 1 2 2 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2
% Query Match Length DB	1536 1536 1536 1536
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Score	1 1535.6 100.0 2 1535.6 100.0 3 1535.6 100.0 4 1535.6 100.0
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GENERAL INFORMATION:
APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH
APPLICANT: LUDWIG INSTITUTE FOR CANCER RESEARCH
APPLICANT: LUDWIG INSTITUTE FOR CANCER FALLOWIG LTD.
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
TITLE OF INVENTION: THEREFOR, FOT/US9/22668B
CURRENT RILING DATE: 1999-09-30
EARLIER PLILORION NUMBER: 60/102,461
EARLIER PLILOM DATE: 1998-11-12
EARLIER FILING DATE: 1998-11-12
EARLIER FILING DATE: 1998-11-13
EARLIER PRILOM DATE: 1998-12-03
EARLIER PRILOM DATE: 1998-12-03
EARLIER PRILOM DATE: 1998-12-18
EARLIER PRILOM DATE: 1999-07-15
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US-10-131-600-4

US-10-31-978-4

US-09-18-42-1

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US-09-172-42-1

US-10-178-42-1

US-10-178-42-2

PCT-US01-43523-285

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PCT-US01-43523-285

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US-09-918-585A-487

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US-09-978-192A-487

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                                                                                             DB 1; Length 1536;
                                                                                                                                             0;
                                                                                                                                             0; Indels
                                                                                          100.0%; Score 1535.6;
llarity 100.0%; Pred. No. 0;
Conservative 0; Mismatches
; TYPE: DNA
; ORGANISM: Homo sapiens
PCT-US99-22668-4
                                                                                             Query Match
Best Local Similarity
Matches 1536; Conserv
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APPLICANT: HELSINKI UNIVERSITY LICENSING LTD.
TITLE OF INVENTION: THEASTAY LICENSING LTD.
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFRENCE: PCT/US99/22669-LUDWIG INST FOR CANCER
CURRENT PRILIGE DATE: 1999-09-30
RARLIER APPLICATION NUMBER: 60/102,461
EARLIER APPLICATION NUMBER: 60/102,461
EARLIER PILING DATE: 1999-09-30
EARLIER PILING DATE: 1999-11-12
EARLIER FILING DATE: 1999-11-12
EARLIER FILING DATE: 1999-12-13
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CGCATCACCACCAGCAGCTCTTGCCCAGAGCTGTGCAGTGCAGTGGCTGATTCTATTAGA 1020
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  CGGGTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATG
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APPLICANT: HELDIN, CARI-Henrik
APPLICANT: BETSHOLTZ, Christer
TITLE OF INVENTION: PLATELET-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT APPLICATION NUMBER: US/09/852,209
CURRENT APPLICATION NUMBER: 09/410,349
FRIOR APPLICATION NUMBER: 60/110,749
FRIOR PILING DATE: 1999-09-30
PRIOR PILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR APPLICATION NUMBER: 60/1135,426
PRIOR APPLICATION NUMBER: 60/114,022
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR APPLICATION NUMBER: 60/144,022
PRIOR PILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PATCHLIN VET: 2.0
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APPLICANT: LEE, Xuri
APPLICANT: PONTEN, Annica
APPLICANT: UTJELA, Marko
APPLICANT: ALITANO, Kari
APPLICANT: OESTWAN, Arne
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ORGANISM: Homo sapiens
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| Sequence 4, Application US/09852209A
| GENERAL INFORMATION
| APPLICANT: ERIKSSON, UIf
| APPLICANT: AASE, Karin
| APPLICANT: DIE, Xuri
| APPLICANT: DUTELA, Marko
| APPLICANT: DUTELA, Marko
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| APPLICANT: DUTELA, Marko
| APPLICANT: DUTELA, Marko
| APPLICANT: DITTALO, Karin
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| FILING DATE: 1999-09-30
| PRIOR FILING DATE: 1999-05-21
| PRIOR FILING DATE: 1999-05-21
| PRIOR FILING DATE: 1999-07-15
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100.0%; Score 1535.6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1536; Conservative 0; Mismatches
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APPLICANT: HELDIN, CAIL-Henrik
APPLICANT: HERDIN, CAIL-Henrik
APPLICANT: HERSHOLTZ, Christer
TITLE OF INVENTION: PLATELE-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: PLATELE-DERIVED GROWTH FACTOR C,
TITLE OF INVENTION: THEREFOR, AND USES THEREOF
FILE REFERENCE: 09-410349-Eriksson et al-1064-44740
CURRENT PRIOR APPLICATION NUMBER: US/09/410,349
PRIOR APPLICATION NUMBER: US/09/410,349
PRIOR APPLICATION NUMBER: 60/108,109
PRIOR APPLICATION NUMBER: 60/110,749
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1998-12-03
PRIOR FILING DATE: 1999-05-21
PRIOR APPLICATION NUMBER: 60/113,002
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-05-21
PRIOR FILING DATE: 1999-07-15
NUMBER OF SEQ ID NOS: 39
SEGFWARE PREDIT VOIL VET: 2.0
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GENERAL INFORMATION:
APPLICANT: BRIKSSON, UIf
APPLICANT: AASE, Karin
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APPLICANT: UUTELA, Marko
APPLICANT: ALITALO, Kari
APPLICANT: OESTMAN, Arne
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LEE, Xuri
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100.0%; Score 1535.6;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1536; Conservative 0; Mismatches
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; Sequence 1, Application US/09184216
; GENERAL INFORMATION:
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Kuo, Sophia S.
; TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
; FILE REFERBNCE: P1122P1
; CURRENT APPLICATION NUMBER: US/09/184,216
; CURRENT FILING DATE: 198e-11-02
; NUMBER OF SEQ ID NOS: 8
; SEQ ID NO 1
; LENGTH: 2825
; TYPE: DNA

COGANISM: Human
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; NAME/KEY: Unknown
; LOCATION: 2689
; OTHER INFORMATION: Any nucleotide
US-09-184-216-1
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US-09-184-216-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 99.8%; Score 1532.6; DB 32; Length 2825; Best Local Similarity 99.9%; Pred. No. 0; Matches 1532; Conservative 1; Mismatches 0; Indels 0;
                                                                                                                                                                                                       Sequence 1, Application US/09723749

| GENERAL INFORMATION:
| APPLICANT: Retrara, Napoleone
| APPLICANT: Retrara, Napoleone
| APPLICANT: Ruo, Sophia S.
| TITLE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
| TILE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
| FILE REFERENCE: P1122P2D1
| CURRENT APPLICATION NUMBER: US/09/723,749
| CURRENT FILING DATE: 1999-03-10
| PRIOR APPLICATION NUMBER: US 09/040,220
| PRIOR FILING DATE: 1998-03-17
| PRIOR PILING DATE: 1998-03-17
| PRIOR PILING DATE: 1998-11-02
| NUMBER OF SEQ ID NOS: 8
| SEQ ID NOS: 8
                                                                                                                 1504 TAAACTIGIGICAIGCIGAIAGGACAGACTGGA 1536
                                                                                                                                 ) LOCATION: 2689
) OTHER INFORMATION: Any nucleotide
US-09-723-749-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Human
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2825
                                                                                                                                                                                          RESULT 9
US-09-723-749-1
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881 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
                                                                                                                                                                                                                                                                                                                                                                                                                        1061 CCATTTTCTGGCCAGGTTGTCTCCTGGTTAAACGCTGTGGTGGGAACTGTGCCTGTTGTC
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                                                                                 484 ATGCTATAACTGCCTTTAGTACCTTGGAAGACCTTATTCGATATCTTGAACCAGAGAT
                                                                                                                                                                                      544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
                                                                                                                                                                                                                                                                                           604 TITITGGAAGAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT
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881 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG 940
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                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 285, Application PC/TUS0143523
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
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                                                                                   Sequence 1, Application US/10178442;
GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Ferrara, Napoleone
ITILE OF INVENTION: POLYPEPTIDES HOMOLOGOUS TO VEGF AND BMPI
TITLE OF INVENTION POLYPEPTIDES HOMOLOGOUS TO VEGF AND EMPI
CURRENT APPLICATION NUMBER: US/10/178,442
CURRENT APPLICATION NUMBER: US/09/265,686
FRIOR PILING DATE: 1999-03-10
FRIOR PILING DATE: 1998-11-02
FRIOR PILING DATE: 1998-11-02
FRIOR PILING DATE: 1998-11-02
FRIOR PILING DATE: 1998-11-02
FRIOR PILING DATE: 1998-11-02
FRIOR APPLICATION NUMBER: US/09/040,220
FRIOR APPLICATION NUMBER: US/09/040,220
FRIOR APPLICATION NUMBER: US/09/040,220
FRIOR APPLICATION NUMBER: US/09/040,220
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FRIOR APPLICATION NUMBER: US/09/040,220
FRIOR APPLICATION NUMBER: US/09/040,220
  1841 TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1873
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
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                                                                 RESULT 10
US-10-178-442-1
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APPLICANT: Gurney, Austin L.
APPLICANT: Sherwood, Steven
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APPLICANT: Watanabe, Colin K
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CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-06-16
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99.8%; Score 1532.6; DB 1; Length 2849;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches 0; Indels 0;
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                                                             Gao, Wei-Qiang
Gerritsen, Mary E.
DeForge, Laura
Desnoyers, Luc
Filvaroff, Ellen
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1027 ACAGCTGCACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACCGATA 1086
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                                                                                                 4 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
                                                0; Gaps
  DB 1; Length 2849;
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  Score 1532.6;
                          Pred. No. 0;
1; Mismatches
99.84;
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Best Local Similarity 99.99
Matches 1532, Conservative
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APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gao, Wel-Qiang
APPLICANT: Gaodwacki, Paul J.
APPLICANT: Gadowacki, Paul J.
APPLICANT: Gadowacki, Paul J.
APPLICANT: Sherwood, Steven
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APPLICANT: Sherwood, Steven
APPLICANT: Sherwood, William
APPLICANT: Change, Daniel
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APPLICANT: Mood, William
APPLICANT: NOWINGER: PCTUS02/24563
CURRENT FILING DATE: 1997-06-10
PRIOR PLILNG DATE: 1997-06-10
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059113
PRIOR APPLICATION NUMBER: 60/059114
PRIOR PLILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/05912
PRIOR PLILING DATE: 1997-09-17
PRIOR PPLILON DATE: 1997-09-17
PRIOR PPLILON NUMBER: 60/05914
PRIOR FILING DATE: 1997-09-17
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                                                                                                                                                                                       1687 CTGTGCAAGTGAGCACCTGATTCCGTTGCCTTGCTTAAACTCTAAAGCTCCATGTCCTGGG 1746
                                                     CCTAAAATCGTATAAAATCTGGATTTTTTTTTTTTTTTGCTCATATTCACATATGTAA 1443
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 285, Application PC/TUS0224563 GENERAL INFORMATION:
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; OTHER INFORMATION: unknown base
PCT-US02-24563-285
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Filvaroff, Ellen
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LENGTH: 2849
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LOCATION: 2715
OTHER INFORMATION: unknown base
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Best Local Similarity 99.99
Matches 1532, Conservative
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APPLICANT: Zhang, Zemin
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OF INVENTION: ACIDS ENCODING THE SAME
FILE REPERENCE: P3330R1C331
CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT APPLICATION NUMBER: PCT/US01/43523
CURRENT FILING DATE: 2002-10-02
PRIOR APPLICATION NUMBER: 60/049911
PRIOR FILING DATE: 1997-08-26
PRIOR FILING DATE: 1997-09-26
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR FILING DATE: 1997-09-17
PRIOR PILING DATE: 1997-09-17
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PRIOR APPLICATION NUMBER: 60/059115
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PRIOR APPLICATION NUMBER: 60/059117
PRIOR APPLICATION NUMBER: 60/05912
                                              GATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT
TAAACTTGTGTCATGCTGATAGGACAGACTGGA 1536
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Tumas, Daniel
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Goddard, Audrey
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Gurney, Austin L.
Sherwood, Steven
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Wood, William
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Filvaroff, Ellen
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PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/059184
PRIOR FILING DATE: 1997-09-17
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PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-18
PRIOR FILING DATE: 1997-09-19
PRIOR FILING DATE: 1997-09-19
PRIOR APPLICATION NUMBER: 60/059588
PRIOR FILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
PRIOR PILING DATE: 1997-09-19
SEQ ID NOS: 550
LENGTH: 2849
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TITLE OF INVENTION: Treating Ocular Diseases; FILE REFERENCE: P2632; CURRENT APPLICATION NUMBER: US/09/267,213; CURRENT FILING DATE: 1999-03-12; NUMBER OF SEQ ID NOS: 41; SEQ ID NO 1; SEQ ID NO 1; LEMETH: 2849; TYPE: DNA; ORGANISM: Homo sapiens
                                                                                                                                                                                                        Query Match
99.8%; Score 1532.6;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1532; Conservative 1; Mismatches
                                                                                                                       FEATURE:
NAME/KEY: unknown
LOCATION: 2715
OTHER INFORMATION: unknown base
US-09-267-213-1
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GENERAL INFORMATION:
APPLICANT: Ferrara, Napoleone
APPLICANT: Goddard, Audrey
APPLICANT: Henzel, William
APPLICANT: Henzel, William
APPLICANT: Henzel, William
APPLICANT: Klein, Robert D.
APPLICANT: Klein, Robert D.
APPLICANT: Kloin, Ivar J.
APPLICANT: Kloin, Robert D.
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APPLICANT: Wood, William I.
TITLE OF INVENTION: Method of Preventing the Death of Retinal Neurons and
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                                                   TCCACAATTGCAATGAATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGG
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SEQ ID NO 487
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ORGANISM: Homo sapiens
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US-10-648-593-58

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US-09-877-066-1

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٠,	Seguence	US-60-487-610-32074	-	201	13.0	200.2	~

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APPLICATE BYSICOL-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS TH
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR MODULATE PROTEIN TYROSINE KINASES AND/OR
TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
TITLE REPERBNCE: D0273 PCT
CURRENT APPLICATION NUMBER: PCT/US03/26491
PRIOR APPLICATION NUMBER: PCT/US03/26491
PRIOR APPLICATION NUMBER: 60/406,385
PRIOR FILING DATE: 2003-08-27
WUMBER OF SEC ID NOS: 557
SOFTWARE: Patentin version 3.2
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               ; Sequence 58, Application PC/TUS0326491; GENERAL INFORMATION:
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ORGANISM: Homo sapiens
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Matches 1531; Conservative
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CORGANISM: Homo sapiens
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Sequence 58, Application US/10648593

Sequence 58, Application US/10648593

Sequence 58, Application US/10648593

GENERAL INFORMATION:

APPLICANT: Bristol-Myers Squibb Company

TITLE OF INVENTION: INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS

TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS

FILE REFERENCE: D0273 NP

CURRENT APPLICATION NUMBER: US/10/648,593

CURRENT FILING DATE: 2003-08-26

PRIOR PILING DATE: 2003-08-27

NUMBER OF SEQ ID NOS: 557

SEQ ID NOS: 557

SEQ ID NOS: 557

SEQ ID NOS: 557
2014 ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGATGAAT 2073
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99.9%; Pred. No. 0;
Live 1; Mismatches 1; Indels 0
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TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF FILE REFERENCE: CL001469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 231
LENGTH: 13007
                                                                                                                                                                                                                                                                                  TYPE: DNA ORGANISM: Homo sapiens
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GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, Honglin: POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    844 TCCTTCAGTTGAGACCAAASACCGGTGTCAGGGGATTGCACAAATCACTCACCGAGGTGG
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TITLE OF INVENTION: NUCLEIC ACID ARRAYS FOR DETECTING GENE EXPRESSION ASSOCIATED WITH
TITLE OF INVENTION: HUMAN OSTEOARTHRITIS AND HUMAN PROTEASES
FILE REFERENCE: AM 10.081
CURRENT APPLICATION NUMBER: US/60/507,511
CURRENT FILING DATE: 2003-10-02
NUMBER OF SEQ ID NOS: 203623
SOFTWARE: PALENTIN version 3.2
SEQ ID NO 2084
LENGTH: 3007
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GENERAL INFORMATION:
APPLICANT: Wyeth
APPLICANT: Mounts, William M
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US-60-507-511-2084
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                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: TANG, Y. TOM
APPLICANT: TANG, HELY
APPLICANT: HILLMAN, Jennifer L.
APPLICANT: COLEY, Neil C.
APPLICANT: GUEGLER, Karl J.
APPLICANT: GUEGLER, Karl J.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: BAUGHN, Mariah R.
APPLICANT: AU-YONG, Janice K.
TITLE OF INVENTION: GROWTH PACTOR RELATED MOLECULES
FILE REFERENCE: PF-0627 USN
CURRENT APPLICATION NUMBER: US/09/830,320A
CURRENT FILING DATE: 2003-04-29
RICR APPLICATION NUMBER: DCT/US99/25458
PRIOR PILING DATE: 1999-10-28
PRIOR PILING DATE: 1998-10-28
PRIOR PILING DATE: 1998-10-28
PRIOR PILING DATE: 1998-10-11
PRIOR APPLICATION NUMBER: US 60/152,216
PRIOR PILING DATE: 1999-05-17
SROIT APPLICATION NUMBER: US 60/172,233
PRIOR FILING DATE: 1999-05-17
SROIT PON SEQ ID NOS: 12
SOFTWARE: PERL PROGRAM
TYPE: DNA
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US-09-830-320A-8
                                                                                                                                                                                                                                                                                                                Sequence 8, Application US/09830320A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                        APPLICANT: INCYTE GENOMICS, INC. APPLICANT: TANG, Y. TOM
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                 484 AIGCIAIAACIGCCITIAGIACCIIGGAAGACCIIIAIICGAIAICIIGAACCAGAGAGAI 543
                                     604 TITITIGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT 663
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                                                                                                                          776 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTG
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                                                                                                        544 GGCAGTTGGACTTAGAAGATCTATATAGGCCAACTTGGCAACTTCTTGGCAAGGCTTTTG
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                                                                ACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAAAGGAACTATGTTGCTATGAAT 1503
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 98.4%; Score 1511; DB 5; Length 1760;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1522; Conservative 1; Mismatches 1; Indels 1; Gaps
RESULT 7

US-09-457-066-1

Sequence 1, Application US/09457066

GENERAL INFORMATION:

APPLICANT: Gao, Zeren

APPLICANT: Hart, Charles E.

APPLICANT: Piddington, Christopher S.

APPLICANT: Sheepard, Paul O.

APPLICANT: Sheemaker, Kimberly E.

APPLICANT: Glibertson, Debra G.

APPLICANT: Glibertson, Debra G.

TITLE OF INVENTION: GROWITH PACTOR HOMOLOG ZVEGP3

FILE REPERRNCE: 98-60

CURRENT FILING DATE: 1999-12-07

NUMBER OF SEQ ID NOS: 50

SOFTWARE: FRSESO for Windows Version 3.0

SECOND 100 1
                                                                                                                                                  1504 TAAACTIGIGICAIGCIGAIAGGACAGACTGGA 1536
                                                                                                                                                                          ; LOCATION: (154)...(1191)
US-09-457-066-1
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LENGTH: 17
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APPLICANT: HATE CHARLES E.
APPLICANT: Gilbertson, Debra G.
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                                                       GENERAL INFORMATION:
APPLICANT: Gilbert, Teresa
APPLICANT: Gilbert, Charles E.
APPLICANT: Sheppard, Faul O.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF4
FILE REFERENCE: 99-19
CURRENT APPLICATION NUMBER: US/09/864,595
PRIOR PILING DATE: 2001-06-06
PRIOR FILING DATE: 2000-05-03
PRIOR FILING DATE: 1999-05-03
PRIOR PILING DATE: 1999-06-03
PRIOR APPLICATION NUMBER: US 09/304,216
PRIOR FILING DATE: 1999-06-03
PRIOR PILING DATE: 1999-06-03
PRIOR FILING DATE: 1999-06-04
PRIOR FILING DATE: 1999-06-05
PRIOR FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 57
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 32
LENGTH: 1760
LENGTH: 1760
LENGTH: 1760
LENGTH: 1760
                              Sequence 32, Application US/09876813 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: (154)...(1191)
US-09-876-813-32
                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA ORGANISM: Homo sapiens
RESULT 8
US-09-876-813-32
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                                                           604 TITITIGGAAGAAAATCCAGAGTGGTGGATCTGAACCTTCTAACAGAGGAGGTAAGATTAT
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us-09-852-209a-4.rnpn

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TYPE: DNA ORGANISM: Artificial Sequence
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SEQ ID NO 50
LENGTH: 1095
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US-09-457-066-50
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                                                                                                                                                                                                                                                        98.4%; Score 1511; DB 6; Length 1760; 99.8%; Pred. No. 0; tive 1; Mismatches 1; Indels 1;
TITLE OF INVENTION: METHODS FOR PROMOTING GROWTH OF BONE, TITLE OF INVENTION: LIGAMENT AND CARTILAGE FILE REFERENCE: 00-12 CURRENT APPLICATION NUMBER: US/10/664,432 CURRENT FILING DATE: 2003-09-19 NUMBER OF SEQ ID NOS: 5 SOFTWARE: FastSEQ for Windows Version 3.0 SEQ ID NO 1 LENGTH: 1760
                                                                                                                                                                                                                                                                            Best Local Similarity 99.8
Matches 1522; Conservative
                                                                                                                                                                                              ; NAME/KEY: CDS
; LOCATION: (154)...(1191)
US-10-664-432-1
                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
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1384 CCTAAAATCGTATAAATCTGGA-TTTTTTTTTTTTTTTGCTCATATTCACATATGTA 1442
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1024 CGTATGCGTTATCTCCATCCTTAATCTCAGTTGTTTGCTTCAAGGACCTTTCATCTTCAG 1083
                                                                                                                                                                                                                                                                                                                                                                           1316 GATTTACAGTGCATTCTGAAAGAGGAGACATCAAACAGAATTAGGAGTTGTGCAACAGCT 1375
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GENERAL INFORMATION:
APPLICANT: Gao, Zerrales E.
APPLICANT: Hart, Charles E.
APPLICANT: Bright, Paul O.
APPLICANT: Shepperd, Paul O.
APPLICANT: Shepperd, Paul O.
APPLICANT: Shepperd, Paul O.
APPLICANT: Shepperd, Paul O.
APPLICANT: Gilbertson, Debra G.
APPLICANT: West, James W.
TITLE OF INVENTION: GROWTH FACTOR HOMOLOG ZVEGF3
FILE REPERBYCE: 98-60
CURRENT FILLING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
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46.9%;
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Best Local Similarity 83.6'
Matches 817, Conservative
                                                                                                                                                                                                                          ; LOCATION: (1049)...(2086)
US-09-457-066-42
                                                                                                                                                                                              ORGANISM: Mus musculus
                                                                                                                                                                                                                   NAME/KEY: CDS
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                                                                                        GTAAATTCCAGTTTTCCAGCAACAAGGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
                                                                                                                GAATTATTACTGTGTCTACTAATGGAAGTATTCACAGCCCAAGGTTTCCTCATACTTATC
                                                                                                                                                    CAAGAAATACGGTCTTGGTATGGAGTTAGTAGCAGTAGAGGAAAATGTATGGATACAAC
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                                      Length 1095
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                                   Query Match 62.2%; Score 955.6; DB 5; Best Local Similarity 99.9%; Pred. No. 5.2e-293; Matches 955; Conservative 1; Mismatches 0;
 ; FEATURE:
; OTHER INFORMATION: Fused
US-09-457-066-50
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Sequence 42, Application US/09457066

GENERAL INFORMATION:
APPLICANT: Gao, Zeren
APPLICANT: Hart, Charles E.
APPLICANT: Hadington, Christopher S.
APPLICANT: Sheemaker, Kimberly E.
APPLICANT: Sheemaker, Kimberly E.
APPLICANT: Sheemaker, Muberly E.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Gilbertson, Debra G.
APPLICANT: Hest, James W.
TITLE OF INVENTION: GROWH PACTOR HOMOLOG ZVI
FILE REFERENCE: 98-60
CURRENT RELIGATION NUMBER: US/09/457,066
CURRENT FILING DATE: 1999-12-07
NUMBER OF SEQ ID NOS: 50
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 42
LENGTH: 3571 셤

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RESULT 13
US-10-664-432-3
i Sequence 3, Application US/10664432
i Sequence 13. Application US/10664432
i GENERAL INFORMATION:
APPLICANT: Hart, Charles E.
TITLE OF INVENTION: METHODS PROMOTING GROWTH OF BONE,
TITLE OF INVENTION: LIGAMENT AND CARTILAGE
FILE REFERENCE: 00-12
CURRENT PAPLICATION UNBER: US/10/664,432
CURRENT FILING DATE: 2003-09-19
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3
LENGTH: 3571
TYPE: DNA
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                                  2031 CTCTGGAACACCACGAGGAATGTGACTGTGTGTGGAGGAAACGCAGGAGGGTAACTGC 2090
                                                                                                                                                    64 GAATTAFTACTGTGTCTACTAATGGAAGTATTCACAGGCCCAAGGTTTCCTCATACTTATC 123
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                   664 ACAGCTGCACCTCGTAACTTCTCAGTGTCCATAAGGGAAGAACTAAAGAGAACGATA 723
                                                                                                                            TCCACAATTGCAATGAATGTCAATGTCCCAAGCAAAGTTACTAAAAAATACCACGAGG 843
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18-09-576-813-34
Sequence 34, Application US/09876813
GENERAL INFORMATION:
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; LOCATION: (1049)...(2086)
US-09-876-813-34
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                                                                 1371 Trigragaagrigaaggaggcccagrgarggaagrgrirfaggacgcrigsrgrigsgaa 1430
                                                                                                                                                                                                                                                                                                                                     1671 GGCAGGTGGACTTGGACAGCCTCTACAAGCCAACATGGCAGCTTTTGGGCAAGGCTTTCC 1730
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244 TIGIAGAAGIIGAGGAACCCAGIGAIGGAACIAIAIIAGGGCGCIGGIGGIGGITCIGGIA 303
                                                                                                                                           CTGTACCAGGAAAACAGATTTCTAAAGGAAATCAAATTAGGATAAGATTTGTATCTGATG 363
                                                                                                                                                                                                                                                                                           364 AATATITICCIICIGAACCAGGGIICIGCAICCACIACAACAIIGICAIGCCACAATICA 423
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2107
964 ATCACCACCAGCAGCTC
                    2091 AGCCTTCGTAGCAGCAC
                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
                                                                                                                                                                                                     SEQ ID NO 19346
LENGTH: 221510
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                                                                                           4 GTAAATTCCAGTTTTCCAGCAACAAGAACAGAACGGAGTACAAGATCCTCAGCATGAGA
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                                                                        Gaps
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                                                 Length 3571;
                                                                     Indels
                                               Score 721; DB 6; L. Pred. No. 4.1e-218; 0; Mismatches 160;
                                                Query Match
Best Local Similarity 83.6%;
Matches 817; Conservative
       NAME/KEY: CDS
LOCATION: (1049)...(2086)
                   ; LOCATION: (1
US-10-664-432-3
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Sequence 19346, Application US/60487610
GENERAL INFORMATION:
APPLICANT: CARGILL, Michele
APPLICANT: HUANG, HONGIL
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
TITLE OF INVENTION: LIVER FIBROSIS IN HEPATITIS C VIRUS-INFECTED SUBJECTS,
TITLE OF INVENTION: METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLOO1469
CURRENT APPLICATION NUMBER: US/60/487,610
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 97101
SOFTWARE: FASESSEQ FOR Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; LOCATION: (1).\(\tilde{\Gamma}\).(221510)
; OTHER INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism US-60-487-610-19346
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) NAME/KEY: misc_feature

; LOCATION: (1)...(221510)

; OTHEN INFORMATION: n = A,T,C or G, or insertion/deletion polymorphism (see Tables 1-

US-60-485-450-11913
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                         214495 TGCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAA 214554
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                                                                                                                                                                                                                                                                                                               APPLICANT: CREGILL,
APPLICANT: CREGILL,
APPLICANT: CHANG, Sheng-Yung
TITLE OF INVENTION: GENERAL PURP
TITLE OF INVENTION: RESPONSE TO INTERFERON TREATMENT IN HEPATITIS C
TITLE OF INVENTION: VIRUS-INPECTED SUBJECTS, METHODS OF DETECTION AND USES
TITLE OF INVENTION: THEREOF
FILE REPERENCE: CL001470
CURRENT APPLICATION NUMBER: US/60/485,450
CURRENT FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 47859
SOFTWARE: REAFESQ for Windows Version 4.0
SEQ ID NO 11913
1423 TGCTCATATTCACATATGTAAACCAGAACATTCTATGTACTACAAACCTGGTTTTTAAAA 1482
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                                                                                          1483 AGGAACTAIGITGCTAIGAATTAAACTIGIGTCATGCTGATAGGACAGACTGGA 1536
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                                                                                                                                                                                                                                                                 ; Sequence 11913, Application US/60485450; GENERAL INFORMATION:
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Best Local Similarity 97.89
Matches 698; Conservative
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                        RESULT 15
US-60-485-450-11913
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Search completed: November 26, 2003, 09:11:07 Job time : 288.211 secs RST4916 A 602627750 603394005 Mus muscu Mus muscu AGENCOURT

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AK042767 Mus muscu
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BC02009 Mus muscu
BQ015321 UI-H-EDI-
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BI911795 60306522
BQ694737 1000880 H
BG430400 602502113
BM827309 K-ESTG099
BUG4825 UI-M-EV0-
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Contact: MGC help desk
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLONTECH
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
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Home sapiens, Similar to platelet-derived growth factor, C
PC041783
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1 (bases 1 to 2826)
Straubberg.R.
Direct Submission
Submitted (23-DEC-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
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CB159806
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AU280428
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                                                                                                                 November 25, 2003, 23:39:26; Search time 2241.28 Seconds (without alignments) 16656.442 Million cell updates/sec
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              GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                    22781392 seqs, 12152238056 residues
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Listing first 45 summaries
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